

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:34:33 ; Search time 32.39 Seconds
(without alignments)
256.730 Million cell updates/sec

Title: US-08-700-737-9

Perfect score: 658

Sequence: 1 QVQLQPGAEIVKPGTSVKL.....DGWDYADYWGQTSVTVS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	533.5	81.1	120	2	B22769		Ig heavy chain V r
2	527.5	80.2	120	2	S41394		Ig heavy chain V r
3	519.5	79.0	116	2	S53751		antibody Fab Jel l
4	516	78.4	138	2	E32513		Ig heavy chain pre
5	515	78.3	123	2	S20646		Ig heavy chain pre
6	514.5	78.2	139	1	MHMS18		Ig heavy chain pre
7	514.5	78.2	287	4	PC4402		peB leader/Ig hea
8	514	78.1	120	2	S25175		Ig heavy chain V r
9	507.5	77.1	141	2	JO0076		Ig heavy chain pre
10	507	77.1	122	2	S20643		Ig heavy chain pre
11	499.5	75.9	117	2	B27563		Ig heavy chain V r
12	498.5	75.8	118	2	C30560		Ig heavy chain V r
13	495	75.2	131	2	A27472		Ig heavy chain pre
14	495	75.2	246	2	S38950		Ig gamma chain - m
15	495	75.2	446	2	S40295		Ig gamma-2a chain
16	492.5	74.8	135	2	A30577		Ig heavy chain pre
17	492.5	74.8	139	2	PS0024		Ig heavy chain pre
18	491.5	74.7	122	2	S24287		Ig heavy chain V r
19	489	74.3	110	2	S21917		Ig gamma chain pre
20	488.5	74.2	126	2	S31930		Ig heavy chain pre
21	487	74.0	136	2	PL0208		Ig heavy chain pre
22	486.5	73.9	131	2	S66537		Ig heavy chain V r
23	484.5	73.6	113	2	S25041		Ig heavy chain V r
24	483.5	73.5	115	2	C27563		Ig heavy chain V r
25	483.5	73.5	136	2	JO0077		Ig heavy chain V r
26	482	73.3	116	2	S55542		Ig heavy chain pre
27	481	73.1	117	2	G45722		Ig heavy chain V r
28	479.5	72.9	120	1	MHMS15		anti-glycoprotein
29	478	72.6	138	1	HVMST7		Ig heavy chain pre

ALIGNMENTS

RESULT 1

B22769

Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996

C:Accession: B22769

R:Dillardrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.

EMBO J. 1, 635-640, 1982.

A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between

A:Reference number: A90971; MUID:84236036

A:Accession: B22769

A:Molecule type: protein

A:Residues: 1-120 <BIL>

A:Note: peptides and unsequenced residues were positioned by homology with the B1-8

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.1%; Score 533.5; DB 2; Length 120;

Matches 102; Conservative 84.3%; Pred. No. 6.5e-40;

Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMHVVKORPGQGLEWIGEDPSSTNTY 60

Db 1 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMHVVKORPGQGLEWIGEDPSSTNTY 60

QY 61 NOKFKGKATLTVDISSTAYMQLSLTSDSAVYCYARGYDGYAIDYWGQTSVTVS 120

Db 61 NOKFKGKATLTVDKPSSTAYMQLSLTSDSAVYCYARGYDGYAIDYWGQTSVTVS 119

QY 121 S 121

Db 120 S 120

RESULT 2

S41394

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C:Accession: S41394

R:Margittes, C.; Gilbert, D.; Brard, F.; Tron, F.

submitted to the EMBL Data Library, January 1994

A:Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti

A:Reference number: S41393

A:Accession: S41394

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <MAR>

A:Cross-references: EMBL:229586; NID:9452354; PIDN:CAA82703.1; PID:g1334080

E32513
Ig heavy chain precursor V region (M122) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C:Accession: E32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUIB:88331394
A:Accession: E32513
A:Molecule type: DNA
A:Residues: 1-138 <KOF>
A:CrossReferences: GB:M20835; NID:g196945; PID:AAA38847.1; PID:g196946
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

A;Accession: B90809

A:Molecule type: DNA
A:Residues: 1-117 <1862>
A:Note: the BI-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten
A:Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R:Dilidrop, R.; Brugemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982.
A:Title: Immunoglobulin v region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026
A:Accession: A22769
A:Molecule type: protein
A:Residues: 20-139 <DI>
A:Note: the v region of the BI-8 delta chain, derived as a spontaneous class switch variant
of the mu chain
C:Genetics: 16/1
A:Introns: 16/1
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <DI>
F:20-139/Product: ig kappa chain v region (BI-8) #status experimental <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:118-124/Region: D segment
F:125-139/Region: J segment (JH2)

Sat Apr 14 08:10:30 2001

us-08-700-737-9.rpr

Db 80 NEKEKATLTVDKPSSTAYMQLSSLTSDSAVYCARCAGPAG-----DYWGQGTTLTVS 134

QY 121 S 121

Db 135 S 135

RESULT 10

S20643

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20643

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A:Reference number: S20639

A:Accession: S20643

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-122 <LOS>

A:Cross-references: EMBL:X6498; NID:g52606; PIDN:CAA46131.1; PID:g52607

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Superfamily: heterotetramer; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 507; DB 2; Length 122;

Best Local Similarity 80.6%; Pred. No. 1.3e-37;

Matches 100; Conservative 6; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVLOQPGAEVLKPGTSSVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNY 60

Db 1 QVLOQXXGAELVKPGASVKLSCKASGYTFYRIYHWKORPGOGLEWIGEDIPSDNTYY 60

QY 61 NOKFKGATLTVDISSSTAYMQLSSLTSDSAVYCARCAGYDGDW----YADYWGQGTSS 116

Db 61 NOKFKGATLTVDKSSSTAYMQLSSLTSDSAVYCARREY--YDLRRGHANDYWGQGTSS 118

QY 117 VTVS 120

Db 119 VTVS 122

RESULT 11

B27563

Ig heavy chain V region (T14) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 23-Jul-1999

C:Accession: B27563

R:Carmack, C.E.; Pincus, S.H.

J. Immunol. 137, 3983-3989, 1986

A:Title: Variable regions of antibodies to synthetic polypeptides. II. Analysis of vari

A:Reference number: A92812; MUID:87059009

A:Accession: B27563

A:Molecule type: DNA

A:Residues: 1-117 <CAR>

A:Cross-references: GB:M14974; NID:g195260; PIDN:AAA38226.1; PID:g195261

A:Note: this sequence was determined from the differentiated gene

A:Note: the authors translated the codon GGT for residue 54 as Ala and TAC for residue 5

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Superfamily: heterotetramer; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

F:12-95/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 499.5; DB 2; Length 117;

Best Local Similarity 78.8%; Pred. No. 5.8e-37;

Matches 93; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 4 LOQPGAEVLKPGTSSVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNYNQK 63

Db 4 LOQPGAEVLKPGASVKLSCKASGYTFYRIYHWKORPGOGLEWIGEDIPSDNSGGTKYNEK 60

QY 64 FKKGATLTVDISSSTAYMQLSSLTSDSAVYCARCAGYDGDWYADYWGQGTSSVTVSS 121

Db 61 FKNKATLTINKPNTAYMQLSSLTSDSAVYCAR-CYDYSYAMDYWGQGTSSVTVSS 117

RESULT 12

C30560

Ig heavy chain V region (35.8.2H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999

C:Accession: C30560

R:Matsuda, T.; Kabat, E.A.

J. Immunol. 142, 863-870, 1989

A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono

A:Reference number: A30560; MUID:89110062

A:Accession: C30560

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MAT>

A:Cross-references: GB:M24270; NID:g195615; PIDN:AAA38371.1; PID:g195616

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Superfamily: heterotetramer; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 498.5; DB 2; Length 118;

Best Local Similarity 80.2%; Pred. No. 7.2e-37;

Matches 97; Conservative 4; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVLKPGTSSVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNY 60

Db 1 QVHLOQSGAEVLKPGASVKLSCKASGYTFYRIYHWKORPGOGLEWIGEDIPSNYTN 60

QY 61 NOKFKGATLTVDISSSTAYMQLSSLTSDSAVYCARCAGYDGDWYADYWGQGTSSVTN 120

Db 61 NOKFKGATLTVDKSSSTAYMQLSSLTSDSAVYCARWGTSW---PAYWGQGTTLTVS 117

QY 121 S 121

Db 118 A 118

RESULT 13

A27472

Ig heavy chain precursor V region (1E9) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-Oct-1996

C:Accession: A27472

R:Liu, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.

Gene 54, 33-40, 1987

A:Title: Expression of mouse:human immunoglobulin heavy-chain cDNA in lymphoid cells

A:Reference number: A27472; MUID:87277430

A:Accession: A27472

A:Molecule type: mRNA

A:Residues: 1-131 <LIU>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:5-54/Region: complementarity-determining 1

F:20-131/Product: Ig heavy chain V region 1E9 #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:69-85/Region: complementarity-determining 2

F:118-125/Region: complementarity-determining 3

Query Match 75.2%; Score 495; DB 2; Length 131;

Best Local Similarity 82.6%; Pred. No. 1.6e-36;

Matches 95; Conservative 3; Mismatches 13; Indels 4; Gaps 2;

QY 1 QVLOQPGAEVLKPGTSSVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNY 60

Db 20 QVLOQPGAEVLKPGASVKLSCKASGYTFYRIYHWKORPGOGLEWIGEDIPSNGRNTY 79


```
Query Match      75.2%; Score 495; DB 2; Length 446;
Best Local Similarity 76.9%; Pred. No. 5.9e-36;
Matches 93; Conservative 10; Mismatches 14; Indels 4; Gaps
```

	QY	1	QVLOOQPAGELVKPGTSVLCKSGKGYGTYTTSYMMHWVKORPQGGLWEIGEDIPSESNTNY	60
			: : : :	
	Dd	1	QIQLOOQSPGLVRPGASVKISCAKSCATFTDYIHVKORPGEGLWGIWIYPGSNTKY	60
			:	
	QY	61	NQFKFKAHLTVDISSTAYMOLSSLTSEDSSAVYVCARGYGWDVAIDYWGOGTSVTVS	120
			:	
	Dd	61	NQFKFKAHLTVDTSSSTAYMOLSSLTSEDSAVYFCARGG----KFAMDYWGCGTSVTVS	116
			:	
	QY	121	S 121	
	Dd	117	S 117	

Search completed: April 13, 2001, 15:36:46
Job time: 133 sec

```

Query Match          75.2%; Score 495; DB 2; Length 246;
Best Local Similarity 76.9%; Pred. No. 3.2e-36;
Matches 93; Conservative 10; Mismatches 14; Indels 4; Gaps 1;

QY 1 OVQLQOPGAELVKPGTSVKLSCKGCGYGTFTSYMHVHWKQRPQGCGLEWIGEDIDPSQNTNY 60
   I:||||| I:||||| I:||||| I:||||| I:||||| I:||||| I:||||| I:|||||
Db 1 QVLQSQSGPELVPRGASVKLSCKASGTYFDYDIHWVKQRPQEGLEWIGWIYPGSGNTKY 60
   I:||||| I:||||| I:||||| I:||||| I:||||| I:||||| I:||||| I:|||||

QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVVYCARGGYDGDWDAIDYWGOGTSTVTS 120
   I:||||| I:||||| I:||||| I:||||| I:||||| I:||||| I:||||| I:|||||
Db 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARGG----KPFANDIYWGOGTSTVTS 116

QY 121 S 121
   |
Db 117 S 117

RESULT 15
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
Submitted to: K. Kleber, S.; Kratzl, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B.
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: Protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region: immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:229/Binding site: carbohydrate (Asn) (covalent) #status experimental

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:35:47 ; Search time 21.32 Seconds
(without alignments)
194.414 Million cell updates/sec

Title: US-08-700-737-9

Perfect score: 658

Sequence: 1 QVQLQPCAEILVKGPTSVKL.....DGWDYADYWGQTSVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	514.5	78.2	139	1	HV07_MOUSE	P01751	mus musculus
2	479.5	72.9	120	1	HV50_MOUSE	P06329	mus musculus
3	478	72.6	138	1	HV48_MOUSE	P03980	mus musculus
4	469.5	71.4	137	1	HV11_MOUSE	P01755	mus musculus
5	469	71.3	140	1	HV02_MOUSE	P01746	mus musculus
6	468	71.1	120	1	HV03_MOUSE	P01747	mus musculus
7	464	70.5	117	1	HV06_MOUSE	P01750	mus musculus
8	452	68.7	117	1	HV09_MOUSE	P01753	mus musculus
9	451	68.5	117	1	HV05_MOUSE	P01749	mus musculus
10	447	67.9	117	1	HV12_MOUSE	P01756	mus musculus
11	447	67.9	121	1	HV01_MOUSE	P01748	mus musculus
12	445	67.6	117	1	HV04_MOUSE	P01745	mus musculus
13	445	67.6	117	1	HV13_MOUSE	P01757	mus musculus
14	441.5	67.1	118	1	HV51_MOUSE	P06330	mus musculus
15	441	67.0	117	1	HV49_MOUSE	P01754	mus musculus
16	440	66.9	117	1	HV10_MOUSE	P01759	mus musculus
17	409	62.2	136	1	HV15_MOUSE	P01758	mus musculus
18	395	60.0	117	1	HV52_MOUSE	P01743	homo sapien
19	383	58.2	117	1	HV14_MOUSE	P23083	homo sapien
20	372.5	56.6	147	1	HV1C_HUMAN	P01812	mus musculus
21	365	55.5	117	1	HV1B_HUMAN	P01808	mus musculus
22	357	54.3	117	1	HV1G_HUMAN	P01741	mus musculus
23	348	52.9	117	1	HV42_MOUSE	P01807	mus musculus
24	347.5	52.8	114	1	HV00_MOUSE	P01811	mus musculus
25	341.5	51.9	119	1	HV38_MOUSE	P01805	rattus norv
26	335	50.9	117	1	HV41_MOUSE	P01809	mus musculus
27	333.5	50.7	119	1	HV37_MOUSE	P01810	mus musculus
28	328	49.8	142	1	HV01_RAT	P06331	homo sapien
29	327	49.7	118	1	HV39_MOUSE	P01771	homo sapien
30	326.5	49.6	136	1	HV16_MOUSE		
31	325.5	49.5	119	1	HV40_MOUSE		
32	325.5	49.5	146	1	HV21_HUMAN		
33	319	48.5	121	1	HV33_HUMAN		

34 316 48.0 125 1 HV1E_HUMAN P06325 homo sapien
35 312 47.4 117 1 HV1A_HUMAN P01742 homo sapien
36 311.5 47.3 122 1 HV3G_MOUSE P01768 homo sapien
37 308 46.8 115 1 HV3K_HUMAN P01801 mus musculus
38 306.5 46.6 126 1 HV30_MOUSE P01772 homo sapien
39 306 46.5 113 1 HV1H_HUMAN P01799 mus musculus
40 305.5 46.4 120 1 HV1D_HUMAN P80421 homo sapien
41 303.5 46.1 124 1 HV35_MOUSE P01760 homo sapien
42 302.5 45.0 111 1 HV27_MOUSE P01804 mus musculus
43 301 45.7 113 1 HV27_MOUSE P01796 mus musculus
44 301 45.7 123 1 HV33_MOUSE P01794 mus musculus
45 300 45.6 115 1 HV33_MOUSE P01802 mus musculus

ALIGNMENTS

RESULT 1
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
RL
CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; J00529; AAA38170.1; -
CC PIR; A02034; MHMS18.
CC InterPro: IPR003006; -
CC Pfam; PF00047; ig; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC DOMAIN 20 49 FRAMEWORK 1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
CC DOMAIN 55 68 FRAMEWORK 2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
CC DOMAIN 86 117 FRAMEWORK 3.
CC DOMAIN 118 124 D SEGMENT.
CC DOMAIN 125 139 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 78.2%; Score 514.5; DB 1; Length 139;
Best Local Similarity 81.0%; Pred. No. 1e-44;
Matches 98; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

```
QY 1 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYMMHWKQRPQGLEWIGTIDPSESNTNY 60
DB 20 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYMMHWKQRPQGLEWIGTIDPSESNTNY 79
QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVVYCARGGYDGMWYDAIDYWGQGTSTVTS 120
DB 80 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVVYCARGGYDGMWYDAIDYWGQGTSTVTS 138
QY 121 S 121
DB 139 S 139
RESULT 2
HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=841182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR InterPro: IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;
```

```
Query Match 72.9%; Score 479.5; DB 1; Length 120;
Best Local Similarity 75.2%; Pred. No. 2.7e-41;
Matches 91; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 1 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYMMHWKQRPQGLEWIGTIDPSESNTNY 60
DB 1 QVLOQPGTGLVLPKPGASVNLSCSKASGYFTSYMMHWIRQRPQGLEWIGTIDPSESNTNY 60
QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVVYCARGGYDGMWYDAIDYWGQGTSTVTS 120
DB 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVVYCARGGYDGMWYDAIDYWGQGTSTVTS 119
QY 121 S 121
DB 120 S 120
RESULT 3
HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR InterPro: IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 72.6%; Score 478; DB 1; Length 138;
Best Local Similarity 74.6%; Pred. No. 4.4e-41;
Matches 91; Conservative 11; Mismatches 16; Indels 4; Gaps 2;

QY 1 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYMMHWKQRPQGLEWIGTIDPSESNTNY 60
DB 20 QVLOQPGAEVLKPGASVNLSCSKASGYFTSYMMHWIRQRPQGLEWIGTIDPSESNTNY 79
QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVVYCARGGYDGMWYDAIDYWGQGTSTVTS 119
DB 80 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVVYCARGGYDGMWYDAIDYWGQGTSTVTS 136
QY 120 S 121
DB 137 SA 138
RESULT 4
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC EMBL: J00539: AAA38172.1; -
DR PIR: A02038: G2MS43.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;
```

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Query Match 71.4%; Score 469.5; DB 1; Length 137;
Best Local Similarity 73.4%; Pred. No. 3.1e-40;
Matches 91; Conservative 7; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYWMHWKQRPQGLEWIGEDPSESNTNY 60
Db 20 QVLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYWMHWKQRPQGLEWIGEDPSESNTNY 79
QY 61 NQKFKGKATLTVDISSTAYMQLSLTSEDSAVYVCARGGYDGDWDYADYWGQGTSTV 117
Db 80 NEHFRSKATLTVDKSSSTAYMQLSLTSEDSAVYVCARGGYDGDWDYADYWGQGTSTV 133
QY 118 TVSS 121
Db 134 TVSS 137
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RESULT 5
HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC EMBL: J00493: AAA38128.1; -
DR PIR: A02028: HVMSG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
```

```
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 71.3%; Score 469; DB 1; Length 140;
Best Local Similarity 73.6%; Pred. No. 3.6e-40;
Matches 89; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYWMHWKQRPQGLEWIGEDPSESNTNY 60
Db 20 QVLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYWMHWKQRPQGLEWIGEDPSESNTNY 79
QY 61 NQKFKGKATLTVDISSTAYMQLSLTSEDSAVYVCARGGYDGDWDYADYWGQGTSTV 120
Db 80 NEKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYVCARGGYDGDWDYADYWGQGTSTV 139
QY 121 S 121
Db 140 S 140
```

```
RESULT 6
HV03_MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotypic response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC PIR: A02028; HVMSG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
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Query Match 71.1%; Score 468; DB 1; Length 120;
Best Local Similarity 74.2%; Pred. No. 3.8e-40;
Matches 89; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 QVLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYWMHWKQRPQGLEWIGEDPSESNTNY 61
Db 1 QVLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYWMHWKQRPQGLEWIGEDPSESNTNY 60
QY 62 QKFKGKATLTVDISSTAYMQLSLTSEDSAVYVCARGGYDGDWDYADYWGQGTSTV 121
Db 61 EKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYVCARGGYDGDWDYADYWGQGTSTV 120

RESULT 7
HV06_MOUSE STANDARD; PRT; 117 AA.
ID HV06_MOUSE
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
```

21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02032; HVMS02.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
Query Match 70.5%; Score 464; DB 1; Length 117;
Best Local Similarity 90.6%; Pred. No. 9.2e-40;
Matches 87; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 2 VOLOQPGAEVLKPGTGVKLSCKGCGYFTTSYWMHWKQPGGLEWIGEDPSESNTYN 61
DB 21 VOLOQPGAEVLKPGTGVKLSCKGCGYFTTSYWMHWKQPGGLEWIGEDPSESNTYN 80
QY 62 QKFKGKATLVDTSSSTAYMOLSLTSEDSAVYYCA 97
DB 81 QKFKGKATLVDTSSSTAYMOLSLTSEDSAVYYCA 116
RESULT 8
HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: B02034; HVMS61.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;
Query Match 68.7%; Score 452; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 1.4e-38;
Matches 84; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 1 QVLOQPGAEVLKPGTGVKLSCKGCGYFTTSYWMHWKQPGGLEWIGEDPSESNTYN 60
DB 20 QVLOQPGAEVLKPGTGVKLSCKGCGYFTTSYWMHWKQPGGLEWIGEDPSESNTYN 79
QY 61 NQKFKGKATLVDTSSSTAYMOLSLTSEDSAVYYCAR 98
DB 80 NQKFKGKATLVDTSSSTAYMOLSLTSEDSAVYYCAR 117
RESULT 9
HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC EMBL; J00536; AAA38605.1; -.
CC PIR; A02031; HVMS3.
CC InterPro: IPR003006; -.
CC Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

```

Query Match      68.5%; Score 451; DB 1; Length 117;
Best Local Similarity 87.8%; Pred. No. 1.8e-38;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSLKSCGYGFTSYMMHWKQRPQGGLEWIGEDIPSESNTNY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 QVQLQPGAEIVKPGTSLKSCGYGFTSYMMHWKQRPQGGLEWIGEDIPSESNTNY 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSDSAVYVCAR 98
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYVCAR 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MMS4E.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match      67.9%; Score 447; DB 1; Length 117;
Best Local Similarity 71.1%; Pred. No. 4.6e-38;
Matches 86; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 1 QVQLQPGAEIVKPGTSLKSCGYGFTSYMMHWKQRPQGGLEWIGEDIPSESNTNY 60
    :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 1 EVQLQSGPELVKPGASVKMSCKASGYFTDYMKWKQSHGKSLGWIGDINPNGGTSY 60
    :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSDSAVYVCARGYDGDWDYDVGQGTSTVTS 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYVCAR----DYDWDYDVGAGCTTIVTS 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 S 121
DB 117 S 117

RESULT 11
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match      67.9%; Score 447; DB 1; Length 121;
Best Local Similarity 69.4%; Pred. No. 4.8e-38;
Matches 84; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSLKSCGYGFTSYMMHWKQRPQGGLEWIGEDIPSESNTNY 60
    :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 1 EAQLQSGAEIVKPGTSLKSCGYGFTSYMMHWKQRPQGGLEWIGEDIPGGGFTNY 60
    :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSDSAVYVCARGYDGDWDYDVGQGTSTVTS 120
    | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
DB 61 NDNLKGRKATLTADTSSTAVYQLSSLTSDSAIVHCARGIYNSPPYFDSKGGQTTIVTS 120
    | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
QY 121 S 121
DB 121 S 121

RESULT 12
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.B.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02030; HVM523.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

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FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 67.6%; Score 445; DB 1; Length 117;
Best Local Similarity 84.7%; Pred. No. 7.2e-38;
Matches 83; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSLVSKLCKGKGYFTSYMMHWVKQRPQGLGEIDPSESNTNY 60
DB 20 QVQLQPGAEIVKPGTSLVSKLCKGKGYFTSYMMHWVKQRPQGLGEIDPSESNTNY 79
QY 61 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYYCAR 98
DB 80 NEKFKSKVTLTVDKSSSTAYTQLSLTSDSAVYYCAR 117

RESULT 13
HV13_MOUSE STANDARD; PRT; 117 AA.
ID HV13_MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MMSJ5.
DR InterPro; IPR003006; .
DR Pfam; PF00047; 19; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 67.6%; Score 445; DB 1; Length 117;
Best Local Similarity 71.9%; Pred. No. 7.2e-38;
Matches 87; Conservative 11; Mismatches 19; Indels 4; Gaps 2;

QY 1 QVQLQPGAEIVKPGTSLVSKLCKGKGYFTSYMMHWVKQRPQGLGEIDPSESNTNY 60
DB 1 EVQLQSGPELVKPGASVKKSCASGYFTDYMMKWVKQSHGKSLGWIGDINPNNGGTSY 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYYCARGYDGYDWDYADYWGQGTSTVTVS 120
DB 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYYCARDRY--WYF--DVMGAGTSTVTVS 116

RESULT 14
HV51_MOUSE STANDARD; PRT; 118 AA.
ID HV51_MOUSE
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AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84182519; PubMed=6201362;
RA Dillard R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MMS38.
DR InterPro; IPR003006; .
DR Pfam; PF00047; 19; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 67.1%; Score 441.5; DB 1; Length 118;
Best Local Similarity 70.5%; Pred. No. 1.6e-37;
Matches 86; Conservative 11; Mismatches 20; Indels 5; Gaps 2;

QY 1 QVQLQPGAEIVKPGTSLVSKLCKGKGYFTSYMMHWVKQRPQGLGEIDPSESNTNY 60
DB 1 EVQLQSGPELVKPGASVKKSCASGYFTDYMMKWVKQSHGKSLGWIGDINPNNGGTSY 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYYCARG-YDGYDWDYADYWGQGTSTVTV 119
DB 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYYCARGYD-----PFDVWGTTGTTVTV 116

RESULT 15
HV49_MOUSE STANDARD; PRT; 117 AA.
ID HV49_MOUSE
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH58 B4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: M13788; AAA38506.1; -
DR PIR: A02035; MHMSB4.
DR InterPro: IPR003006; -
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 67.0%; Score 441; DB 1; Length 117;
Best Local Similarity 84.5%; Pred. No. 1.8e-37;
Matches 82; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
Qy 2 VOLQPGAEVLVPGTSVKLSCKGYGYTFTSYMMHWVKRPGGLEWIGEIDPSESNTNYN 61
Db 21 VOLQPGAEVLVPGASVKLSCKASGYTFTSYMMHWVKRPGGLEWIGNIDPNSGGTKYN 80
Qy 62 QKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCAR 98
Db 81 EKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYYCTR 117

Search completed: April 13, 2001, 15:40:18
Job time: 271 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:35:28 ; Search time 56.51 Seconds
(without alignments)
250.967 Million cell updates/sec

Title: US-08-700-737-9
Perfect score: 658
Sequence: 1 QVQLQPGAEVLKPGTGVKL.....DGWDYALDYWGQTSVTSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-unclassified:*
- 13: sp-vertebrate:*
- 14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	71.9	117	11 Q9QXE9	Q9QXE9 mus musculus
2	464.5	70.6	110	11 Q9JL77	Q9JL77 mus musculus
3	462.5	70.3	114	11 Q9JL81	Q9JL81 mus musculus
4	459	69.8	117	11 Q9QXF0	Q9QXF0 mus musculus
5	458.5	69.7	118	11 Q9ZIC4	Q9ZIC4 mus musculus
6	442.5	67.2	109	11 Q9JL75	Q9JL75 mus musculus
7	437	66.4	117	11 Q9ZIC6	Q9ZIC6 mus musculus
8	414.5	63.0	124	4 Q9UL92	Q9UL92 homo sapien
9	414	62.9	119	4 Q9UL94	Q9UL94 homo sapien
10	412.5	62.7	110	11 Q9JL83	Q9JL83 mus musculus
11	390	59.3	125	4 Q9UL95	Q9UL95 homo sapien
12	386	58.7	109	11 Q9JL85	Q9JL85 mus musculus
13	356.5	54.2	116	4 Q9UL89	Q9UL89 homo sapien
14	353.5	53.7	298	11 Q9QXF0	Q9QXF0 mus musculus
15	352	53.5	150	4 Q9Y298	Q9Y298 homo sapien
16	349	53.0	157	4 Q95978	Q95978 homo sapien
17	323	49.1	116	4 Q9UL93	Q9UL93 homo sapien
18	317	48.2	113	4 Q9UL90	Q9UL90 homo sapien
19	313.5	47.6	147	4 Q9Y509	Q9Y509 homo sapien

20	301.5	45.8	118	4 Q9UL91	Q9UL91 homo sapien
21	301	45.7	131	4 Q9UL88	Q9UL88 homo sapien
22	300	45.6	121	4 Q9UL71	Q9UL71 homo sapien
23	294.5	44.8	122	4 Q9UL84	Q9UL84 homo sapien
24	291	44.2	119	4 Q9UL73	Q9UL73 homo sapien
25	284.5	43.2	118	4 Q9UL72	Q9UL72 homo sapien
26	278.5	42.3	437	11 Q9JL44	Q9JL44 mus musculus
27	278	42.2	102	11 Q9JL79	Q9JL79 mus musculus
28	275.5	41.9	124	6 Q9N0W6	Q9N0W6 oryctolagus
29	273.5	41.6	124	6 Q9N0W4	Q9N0W4 oryctolagus
30	271.5	41.3	150	4 Q95973	Q95973 homo sapien
31	265	40.3	95	4 Q9UL86	Q9UL86 homo sapien
32	253	38.4	112	4 Q9UGP3	Q9UGP3 homo sapien
33	252	38.3	104	4 Q9UL87	Q9UL87 homo sapien
34	239.5	36.4	122	4 Q9UL75	Q9UL75 homo sapien
35	216	32.8	121	4 Q9UL96	Q9UL96 homo sapien
36	212	32.2	82	4 Q95729	Q95729 homo sapien
37	203	30.9	88	4 Q95737	Q95737 homo sapien
38	202	30.7	76	4 Q95742	Q95742 homo sapien
39	199	30.2	118	4 Q9UL74	Q9UL74 homo sapien
40	196	29.8	77	4 Q95741	Q95741 homo sapien
41	193.5	29.4	416	4 Q9NPP6	Q9NPP6 homo sapien
42	188.5	28.6	77	4 Q95726	Q95726 homo sapien
43	188.5	28.6	81	4 Q95719	Q95719 homo sapien
44	187.5	28.5	78	4 Q95730	Q95730 homo sapien
45	187	28.4	77	4 Q95728	Q95728 homo sapien

ALIGNMENTS

RESULT 1

Q9QXE9 ID Q9QXE9 PRELIMINARY; PRT; 117 AA.
AC Q9QXE9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225174; CAB65237.1; -
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 71.9%; Score 473; DB 11; Length 117;
Best Local Similarity 75.2%; Pred. No. 4.2e-42;
Matches 91; Conservative 10; Mismatches 16; Indels 4; Caps 1;

Qy 1 QVQLQPGAEVLKPGTGVKLSKCGYGTFTSYMMHWKQRPQCGLEWIGETDPSKNTNY 60
Db 1 EVQLQSGPELVKPGASVKMSCKASGFTFTDYMKWKQSHGKSLWIGDINPANGTST 60
Qy 61 NQKFKGKATLTVDISSTAYMQLSLTSSEDSAVYYCARGGYDGDWDYATDYWGQTSVTVS 120
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSSEDSAVYYCARDRY-----YAMDYWGQTSVTVS 116
Qy 121 S 121
Db 117 S 117

RESULT 2

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Q9JL77
ID Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206029; AAF69327.1; -.
FT NON_TER 1
FT NON_TER 110 110
FT SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 70.6%; Score 464.5; DB 11; Length 110;
Best Local Similarity 79.3%; Pred. No. 3e-41;
Matches 88; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 11 LVKPGTSVKLSCKGYGTYFTSYMHVHKQPPGOGLEWIGEDIPSESTNYNOKFKGKATL 70
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 LVKPGASVKLSCKASGYFTTSYMHVAKQPPGOGLEWIGEDIPSESTNYNOKFKGKATL 62
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 71 TVDISSTAYMQLSSLTSEDSAVYICARGYDGYDWDYDAIDYWGQTSVTSS 121
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 TVDTSSSTAYVDLSLTSEDSAVYICAR---QRRNAMYDYGQTSVTSS 110
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
Q9JL81
ID Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206025; AAF69323.1; -.
FT NON_TER 1
FT NON_TER 114 114
FT SEQUENCE 114 AA; 12829 MW; 404885FDE6A56F8 CRC64;

Query Match 70.3%; Score 462.5; DB 11; Length 114;
Best Local Similarity 77.9%; Pred. No. 5e-41;
Matches 88; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 10 ELVKPGTSVKLSCKGYGTYFTSYMHVHKQPPGOGLEWIGEDIPSESTNYNOKFKGKAT 69
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 QLVKPGASVKLSCKASGYFTSYMHVHKQPPGOGLEWIGEDIPSESTNYNOKFKGKAT 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 70 LTVDISSTAYMQLSSLTSEDSAVYICARGYDGYDWDYDAIDYWGQTSVTSS 121
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 LTVDKSSSTAYMQLSSLTSEDSAVYICARSNYIGSSLYYFYDYGQGTTLTVSS 114
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 4
Q9QXF0
ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 69.8%; Score 459; DB 11; Length 117;
Best Local Similarity 72.7%; Pred. No. 1.2e-40;
Matches 88; Conservative 11; Mismatches 18; Indels 4; Gaps 1;

QY 1 QVLOQPGALVKPGTSVKLSCKGYGTYFTSYMHVHKQPPGOGLEWIGEDIPSESTNY 60
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVLOQSGPLVKPGASVKMSCKASGYTDDYMKVWKQSHGSKLEWIGDINPNGGTSY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARGYDGYDWDYDAIDYWGQTSVTSS 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYICARDK---DYFYDYGQGTTLTVS 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 S 121
Db 117 S 117

RESULT 5
Q9ZIC4
ID Q9ZIC4 PRELIMINARY; PRT; 118 AA.
AC Q9ZIC4
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 118 118
FT SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 69.7%; Score 458.5; DB 11; Length 118;

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Best Local Similarity 71.8%; Pred. No. 1.4e-40;
Matches 89; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGCGYFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
DB 1 QVQVQSGAELAPWASVKLSCKASGYFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCAR---GGYDGDWDYADYWGQGTSTV 117
DB 61 TQKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARRTVGGY-----FDYWGQGTTL 114
QY 118 TVSS 121
DB 115 TVSS 118

RESULT 6
Q9JL75
ID Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
REMBL; AF206031; AAF69329.1; -;
FT NON_TER 1
FT NON_TER 109
FT SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 67.2%; Score 442.5; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 5.8e-39;
Matches 86; Conservative 8; Mismatches 14; Indels 5; Gaps 2;

QY 10 ELVKPGTSVKLSCKGCGYFTSYMMHWVKQRPQGGLWIGIDPSESNTNYNKKFKGKAT 69
DB 1 ELVKPGASVAMSKASGYFTSYMMHWVKQRPQGGLWIGIYINPDGTYNKKFKGKAT 60
QY 70 LTVDISSTAYMQLSSLTSEDSAVYYCAR---GGYDGDWDYADYWGQGTSTVSS 121
DB 61 LTSDKSSSTAYMQLSSLTSEDSAVYYCARDGNRGP-----DYWGQGTTLVSS 109

RESULT 7
Q9Z1C6
ID Q9Z1C6 PRELIMINARY; PRT; 117 AA.
AC Q9Z1C6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Watis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
19G2/G4 constant regions block human leukocyte binding to porcine

endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
REMBL; U78799; AAD00291.1; -;
INTERPRO; IPR003006; -;
PFAM; PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 117
FT SEQUENCE 117 AA; 13122 MW; 4F65B193APB77E5B CRC64;

Query Match 66.4%; Score 437; DB 11; Length 117;
Best Local Similarity 70.2%; Pred. No. 2.4e-38;
Matches 85; Conservative 8; Mismatches 24; Indels 4; Gaps 2;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGCGYFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
DB 1 QVQLQSGPOLVRPGTSVKLSCKASGYFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGYDGDWDYADYWGQGTSTVSS 120
DB 61 NQRLKDKAILTVDKSSNTAYMQLSSLTSEDSAVYYCTRGEV-SW---FAYWGQGTTLVSS 116
QY 121 S 121
DB 117 A 117

RESULT 8
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
REMBL; AF035022; AAD56258.1; -;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
REMBL; AF035022; AAD56258.1; -;
INTERPRO; IPR003006; -;
PFAM; PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 124
FT SEQUENCE 124 AA; 13580 MW; 1BAAAACBD96ACD2A2 CRC64;

Query Match 63.0%; Score 414.5; DB 4; Length 124;
Best Local Similarity 64.5%; Pred. No. 5.7e-36;
Matches 80; Conservative 17; Mismatches 24; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGCGYFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
DB 1 EVLVESGAELKPGASVKLSCKASGYFTSYMMHWVKQRPQGGLWIGINFPSSGTSY 60
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGYDGDWDY---IDYWGQGTSTV 117
DB 61 AQKFGQGRVTMTDSTSTVYMEELSSLTSEDSAVYYCARGLYVVVPAAFSRFDYWGQGTTLV 120
QY 118 TVSS 121
DB 121 TVSS 124

RESULT 9

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Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13664F5345F4A16E CRC64;

Query Match 62.9%; Score 414; DB 4; Length 119;
Best Local Similarity 65.6%; Pred. No. 6, le-36;
Matches 80; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

QY 1 QVLOQPGAELVKPGTSVKLSCKGTYFTSYMMHWKQPGQGLEWIGEIDPSESNTNY 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVOLVESGAELVKPGTSVKLSCKGTYFTSYMMHWKQPGQGLEWIGWNPNSWTNY 60
QY 61 NQKFKGKATLTVDISSSTAYMOLSLTSDSAVYCARGYDG-WDYAIDYWGQTSVTV 119
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
61 AQKQGVGRVMTTRDTTISTAYMELSLRLSDTAVYCARGGGRGLW---FDPWGQGLTVTV 117
QY 120 SS 121
Db ||
118 SS 119

RESULT 10
Q9JL83
ID Q9JL83 PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206023; AAF69023.1; -
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 62.7%; Score 412.5; DB 11; Length 110;
Best Local Similarity 70.5%; Pred. No. 8e-36;
Matches 79; Conservative 8; Mismatches 22; Indels 3; Gaps 1;

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```

QY 10 ELVKPGTSVKLSCKGTYFTSYMMHWKQPGQGLEWIGEIDPSESNTNYNOKFKGKAT 69
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
2 ELVKPGASVKISCKASGYTFSNSMNMWVKLRPGQGLEWIGRIYPGDGYANGKFKGKAT 61

QY 70 LTVDISSTAYMOLSLTSDSAVYCARGYDGWDYDIDYWGQTSVTVSS 121
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
62 LTPADSSSTAYMOLSLTSDSAVYFCAR---SNNDVRFAYWGQGLTVTVSA 110

RESULT 11
Q9UL95 PRELIMINARY; PRT; 125 AA.
ID Q9UL95;
AC Q9UL95;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 59.3%; Score 390; DB 4; Length 125;
Best Local Similarity 60.0%; Pred. No. 2, le-33;
Matches 75; Conservative 16; Mismatches 30; Indels 4; Gaps 1;

QY 1 QVLOQPGAELVKPGTSVKLSCKGTYFTSYMMHWKQPGQGLEWIGEIDPSESNTNY 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
1 EVOLVESGAELVKPGTSVKLSCKGTYFTSYMMHWKQPGQGLEWIGWNPNSGTNY 60

QY 61 NQKFKGKATLTVDISSSTAYMOLSLTSDSAVYCAR---GGYDGYDIDYWGQGS 116
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
61 AQKQGVGRVMTTRDTTISTAYMELSLRLSDTAVYCARSGGGGRTAAAGDAFDWQGTGM 120

QY 117 VTVSS 121
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
121 VTVSS 125

RESULT 12
Q9JL85 PRELIMINARY; PRT; 109 AA.
ID Q9JL85;
AC Q9JL85;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF206021; AAF69319.1; --
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match
Best Local Similarity 58.7%; Score 386; DB 11; Length 109;
Matches 73; Conservative 13; Mismatches 23; Indels 4; Gaps 1;

QY 9 AELVKPGTSVKLSCKGYGTYFTSYMMHWKQPGGLEWIGEIDPSESNTNYNQKFKGA 68
      ||||| ||||| : : ||||| ||||| ||||| : : |||||
Db 1 AELVKPGASVKLSCTASGTNIEDTYMMHWKQPGGLEWIGRIDPCHSKYDPKFGKA 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 69 TLTVDISSTAYMOLSSLTSDSAVYVCARGYDGDWDYDAIDYWGQTSVTYSS 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TITSTSSNTAYLQLSSLTSDTAVYICVRKG----AVFDDYWGQGTALTYS 109
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; --
DR INTERPRO; IPR003006; --
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match
Best Local Similarity 54.2%; Score 356.5; DB 4; Length 116;
Matches 70; Conservative 16; Mismatches 29; Indels 1; Gaps 1;

QY 6 QPGAELVKPGTSVKLSCKGYGTYFTSYMMHWKQPGGLEWIGEIDPSESNTNYNQKFK 65
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 QSGAEVKKPGSSVKRSCKASGCTSSVAISVRAQPGGLEWGRITPILGIANAQKQF 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 66 GKATLTVDISSTAYMOLSSLTSDSAVYVCARGYDGDWDYDAIDYWGQTSVTYSS 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 GRVTITADKSTAYMELSSLRSEDATVYVCASSNWGPYWFDLWGRGLTIVTSS 116
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CN 8 SCFV.
CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

Query Match
Best Local Similarity 53.5%; Score 352; DB 4; Length 150;
Matches 69; Conservative 14; Mismatches 34; Indels 4; Gaps 1;

QY 1 QVQLQPGAGLVKPGTSVKLSCKGYGTYFTSYMMHWKQPGGLEWIGEIDPSESNTNY 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 20 QVQLVQSGAEVKKPGASVKVSCKVSGYTLITELPVHVGQAPGKGLWVGSFDPESGESIY 79
Qy 61 NQKFKGKATLTVDISSSTAYMOLSSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSTVYS 120
Db 80 AREFOGSVMTADTSTDIAYMELSSLRSDDTAVYYCAVDPDP- ---AFDIWGQGTMTVYS 135
Qy 121 S 121
Db 136 S 136

Search completed: April 13, 2001, 15:39:52
Job time: 264 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: April 13, 2001, 15:33:41 ; Search time 57.59 seconds
(without alignments)
120.103 Million cell updates/sec

Title: US-08-700-737-9

Perfect score: 658

Sequence: 1 QVQLQPGAEIVRPGTSVKL.....DGWDYIDYWGQTSVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq_0401:*

- 1: /SIDSL1/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL1/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL1/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL1/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL1/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL1/gcgdata/geneseq/geneseq/AA1985.DAT:*
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- 14: /SIDSL1/gcgdata/geneseq/geneseq/AA1993.DAT:*
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- 19: /SIDSL1/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSL1/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL1/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSL1/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	100.0	140	19 W53815	Murine Act-1 heavy
2	658	100.0	144	19 W53816	Consensus protein
3	646	98.2	137	19 W53818	Protein sequence o
4	569	86.5	180	19 W53813	Heavy chain of a h
5	538	81.8	119	18 W07436	Anti-DNA antibody
6	536	81.5	119	16 R79863	Anti-EGFR antibody
7	523	79.5	464	19 W83041	Anti-Fas MAb HFE7A
8	523	79.5	464	21 B14747	Mouse anti-Fas ant
9	523	79.5	464	21 W90897	Murine anti-Fas an
10	520.5	79.1	122	16 R84555	B-cell lymphoma CH
11	520	79.0	119	16 R79861	Anti-EGFR antibody

12	520	79.0	445	16 R76085	Mab 55.1 heavy cha
13	520	79.0	464	16 R76088	Mab 55.1 heavy cha
14	518.5	78.8	118	18 W27122	Murine antibody he
15	517.5	78.6	269	15 R54756	PRAS111 between HI
16	517.5	78.6	269	15 R56482	ScFv PRAS107 and p
17	517.5	78.6	402	15 R56485	ScFv PRAS110 and p
18	517.5	78.6	435	15 R56485	ScFv PRAS108 and p
19	517	78.6	288	20 W82743	Fusion protein PNG
20	517	78.6	673	20 W82742	Plasmid PNG4/55.1s
21	516.5	78.5	120	15 R47493	Murine anti-CD18 A
22	513	78.0	119	18 W01578	Lead binding Mab 8
23	511	77.7	136	8 P70624	Sequence encoded b
24	511	77.7	136	18 W10584	Anti-hepatitis B h
25	511	77.7	136	18 W16340	Mouse-human chimae
26	511	77.7	136	18 W10239	Chimeric anti-hepa
27	511	77.7	136	19 W47510	Human anti-hepatit
28	511	77.7	136	19 W41054	Human anti-hepatit
29	511	77.7	136	19 W47517	Human anti-hepatit
30	511	77.7	136	20 W89535	Chimeric anti-hepa
31	510.5	77.6	256	13 R22568	ScFvB18 construct.
32	510.5	77.6	256	13 R22583	ScFvB18 construct
33	510.5	77.6	256	13 R22584	ScFvB18 construct
34	510.5	77.6	256	13 R22585	ScFvB18 construct
35	510.5	77.6	256	13 R22586	ScFvB18 construct
36	510.5	77.6	256	13 R22587	ScFvB18 construct
37	509.5	77.4	428	18 W24027	Single chain anti9
38	509.5	77.4	443	18 W24025	Single chain anti9
39	509.5	77.4	465	16 R66758	Anti-tobacco mosai
40	508	77.2	140	13 R27049	VH425 antibody clo
41	507	77.1	117	17 R88716	Mouse antibody hea
42	506.5	77.0	256	13 R22582	ScFvB18 construct
43	506.5	77.0	415	15 R56484	ScFv PRAS109 and p
44	505	76.7	119	21 Y92156	Murine 13B8 heavy
45	502.5	76.4	240	16 R85495	ScFv(FWP51). Synt

ALIGNMENTS

RESULT 1

W53815
ID W53815 standard; Protein; 140 AA.

XX W53815;

XX 14-JUL-1998 (first entry)

XX Murine Act-1 heavy chain variable region.

XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;

XX Muscosal addressin cell adhesion molecule-1; MadCAM-1;

XX humanised antibody; murine antigen binding region; inhibition;

XX leukocyte infiltration of tissue; treatment; inflammatory disease;

XX inflammatory bowel disease.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note= "signal peptide"

FT Protein /note= "mature protein"

XX W09806248-A2.

XX 19-FEB-1998.

XX 06-AUG-1997; 97WO-US13884.

XX 15-AUG-1996; 96US-0700737.

XX (LEUK-) LEUKOSITE INC.

Db 20 qvqlqpqaelvkpatsvklscckgygtyftsymhwkqrpqgglwlgelidpsesntny 79
 QY 61 NQKFKGKATLTVDISSRAYMOLSLTSDSAVYVCARGYDGYDAIDYWGQGTSVTVS 120
 Db 80 nqkfgkatltvdissstaysmqlsltsedsavyyccargydgwdyaidywgqgtsvts 139
 QY 121 S 121
 Db 140 s 140

RESULT 3
 W53818
 ID W53818 standard; Protein: 137 AA.
 AC W53818;
 XX
 XX
 DT 14-JUL-1998 (first entry)
 DE
 DE Protein sequence of murine variable heavy chain region of clone H2B#34.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 OS
 OS Mus sp.
 OS
 XX
 PN W09806248-A2.
 XX
 PD 19-FEB-1998.
 XX
 PE 06-AUG-1997; 97WO-US13884.
 XX
 PR 15-AUG-1996; 96US-0700737.
 XX
 PA (LEUK-) LEUKOSITE INC.
 XX
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX
 DR WPI; 1998-159172/14.
 DR N-PSDB; V20089.
 XX
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX
 PS Example 1; Fig 2; 145pp; English.
 XX
 CC The present sequence represents the amino acid sequence comprising the
 CC variable region of murine Act-1 antibody determined from clone H2B#34.
 CC Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin
 CC cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular
 CC integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
 CC to MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. The present sequence was used to construct chimeric,
 CC humanised Act-1 antibodies, which contain murine antigen binding regions.
 CC The humanised immunoglobulin can be used to inhibit the interaction of
 CC cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7.
 CC It can be used for inhibiting leukocyte infiltration of tissues, e.g. for
 CC treating inflammatory diseases such as inflammatory bowel disease. The
 CC immunoglobulin can also be used for detection, isolation and diagnosis.
 XX
 SQ Sequence 137 AA;

Query Match 98.2%; Score 646; DB 19; Length 137;
 Best Local Similarity 100.0%; Pred. No. 3-2e-46;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQOPGAELVKPQTSVKLSCKGYGTYFTSYMHWKQRPQGLWIGELIDPSSENTNY 60

Db 20 qvqlqpqaelvkpatsvklscckgygtyftsymhwkqrpqgglwlgelidpsesntny 79
 QY 61 NQKFKGKATLTVDISSRAYMOLSLTSDSAVYVCARGYDGYDAIDYWGQGTSVTVS 118
 Db 80 nqkfgkatltvdissstaysmqlsltsedsavyyccargydgwdyaidywgqgtsvts 137

RESULT 4
 W53813
 ID W53813 standard; Protein: 180 AA.
 AC W53813;
 XX
 XX
 DT 14-JUL-1998 (first entry)
 DE
 DE Heavy chain of a humanised murine Act-1 antibody.
 XX
 XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 OS
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..180
 FT /note= "mature protein"
 XX
 PN W09806248-A2.
 XX
 PD 19-FEB-1998.
 XX
 PE 06-AUG-1997; 97WO-US13884.
 XX
 PR 15-AUG-1996; 96US-0700737.
 XX
 PA (LEUK-) LEUKOSITE INC.
 XX
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX
 DR WPI; 1998-159172/14.
 DR N-PSDB; V20076.
 XX
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX
 PS Claim 20; Fig 11; 145pp; English.
 XX
 CC The present sequence represents the heavy chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 XX
 SQ Sequence 180 AA;

Query Match 86.5%; Score 569; DB 19; Length 180;
 Best Local Similarity 85.1%; Pred. No. 8.8e-40;

Matches 103; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLQPGAEELVKPGTSVKLSCKGSGYGTFTSYWMHWKORPGGLEWIGEIDPSESNTNY 60
 DB 20 QVQLVDSGAEVLRPGASVKLSCKGSGYGTFTSYWMHWKORPGGLEWIGEIDPSESNTNY 79
 QY 61 NQKFKGKATLTVDISSSTAYMQLSSTSEDSAVYICARGYGWDYVADYWGQGTSTVTVS 120
 DB 80 NQKFKGRVLTVDISASTAYMEISSLRSDTAVYICARGYGWDYVADYWGQGTSTVTVS 139
 QY 121 S 121
 DB 140 S 140

RESULT 5
 W07436
 ID W07436 standard; Protein; 119 AA.

XX AC W07436;

XX DT 12-AUG-1997 (first entry)

XX DE Anti-DNA antibody 9f11 group heavy chain variable region.

XX KW Heavy chain; variable region; anti-DNA; monoclonal; antibody;
 KW 9f11 group; hairpin; diagnosis; inflammatory glomerulonephritis;
 KW systemic lupus erythematosus; screening; treatment; prevention;
 KW SLE; disease; consensus; putative.

XX OS Synthetic.

XX FH Key
 FT Region 1..30
 FT /label= framework_I
 FT Region 31..35
 FT /label= CDR_I
 FT Region 36..49
 FT /label= framework_II
 FT Region 50..66
 FT /label= CDR_II
 FT Region 67..98
 FT /label= framework_III
 FT Region 99..108
 FT /label= CDR_III
 FT Region 109..119
 FT /label= J_region
 FT Misc-difference 7
 FT /note= "encoded by CCT"

XX W09636361-A1.

XX PD 21-NOV-1996.

XX PF 16-MAY-1996; 96WO-US07113.

XX PR 18-MAY-1995; 95US-0443540.

XX PA (UNMI) UNIV MICHIGAN.

XX PI Glick GD, Swanson PC;

XX DR WPI; 1997-011854/01.

XX DR N-PSDB; T43805.

XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
 PT develop prods. for diagnosis and treatment of disorders, e.g.
 PT glomerulonephritis or systemic lupus erythematosus

XX PS Example; Fig 9; 102pp; English.

XX CC The present sequence is the heavy chain variable region of the
 CC group 9f11 putative consensus anti-DNA monoclonal antibody (Mab),

CC which has a high affinity for single stranded DNA, low or no
 CC affinity for double stranded DNA and specifically binds a DNA
 CC hairpin. The Mab can be used to diagnose disorders associated with the
 CC pathological complexation of DNA, e.g. inflammatory
 CC glomerulonephritis and systemic lupus erythematosus. It can also be
 CC used to generate reagents to screen for pharmaceutical agents, and
 CC treat and/or prevent an above disorder.
 CC The sequence was derived by aligning homologous anti-DNA Mab,
 CC whose sequences have been published, as well as several Mab of
 CC other specificities obtained from a database search.

XX Sequence 119 AA;

Query Match 81.8%; Score 538; DB 18; Length 119;

Best Local Similarity 85.4%; Pred. NO. 2e-37;

Matches 105; Conservative 5; Mismatches 7; Indels 6; Gaps: 2;

QY 1 QVQLQPGAEELVKPGTSVKLSCKGSGYGTFTSYWMHWKORPGGLEWIGEIDPSESNTNY 60

DB 1 QVQLQPGAEELVKPGASVKLSCKGSGYGTFTSYWMHWKORPGGLEWIGEIDPSESNTNY 60

QY 61 NQKFKGKATLTVDISSSTAYMQLSSTSEDSAVYICARG--GYDGMVYADYWGQGTSTV 118

DB 61 NQKFKGKATLTVDKSSSTAYMQLSSTSEDSAVYICARGRLRY----fandywgrgtsvt 116

QY 119 VSS 121

DB 117 vss 119

RESULT 6

R79863
 ID R79863 standard; Protein; 119 AA.

XX AC R79863;

XX DT 02-JUL-1996 (first entry)

XX DE Anti-EGFR antibody heavy chain variable region (Clone L3 11D).

XX KW Single chain antibody; antibody; epidermal growth factor receptor;

XX EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;

XX KW assessment; phage antibody library.

XX OS Mus musculus.

XX PN W09525167-A1.

XX PD 21-SEP-1995.

XX PF 16-MAR-1995; 95WO-EP00978.

XX PR 02-DEC-1994; 94EP-0118970.

XX PR 17-MAR-1994; 94EP-0104160.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Adnan J, Ansell KH, Bendig MM, Biasco F, Gnessow D;

XX PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;

XX DR WPI; 1995-336972/43.

XX DR N-PSDB; T04016.

XX Anti-EGFR antibodies and single chain Fv antibody fragments -
 PT obtained from phage-antibody libraries, useful for diagnosis and
 PT therapy of tumours

XX PS Claim 4; Page 53; 93pp; English.

XX Anti-epidermal growth factor receptor (EGFR). single chain antibodies
 CC and antibodies constructed from anti-EGFR antibody fragments can be
 CC used for diagnosis of tumours and assessment of tumour growth in

CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See T04011-T04026 and
 CC R79858-R79873)
 XX
 SQ Sequence 119 AA;

Query Match 81.5%; Score 536; DB 16; Length 119;
 Best Local Similarity 85.1%; Pred. No. 3e-37;
 Matches 103; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
 QY 1 QVQLQPGAEIVKPGTSVKLSCKGCGYGTFTSYMMHWVKQRPQGGLWGEIDPSESNTNY 60
 DB 1 :||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 1 evqlqsgaelvpgasvksckasgyftfswmhwkqrpqgglwgeidpsdsytny 60
 QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDYVYCARGYDGDYDAIDYWGQGTSTVTS 120
 DB 61 :||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 1 ngkfkgtatltvdksstaysmqlssltedsavyycarsdygshf--dywgqgttvtvs 118
 QY 121 \$ 121
 DB 119 s 119

RESULT 7
 W83041 ID W83041 standard; Protein: 464 AA.
 AC W83041;
 DT 15-MAR-1999 (first entry)
 DE Anti-Fas MAB HFE7A heavy chain.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 CDR.

XX Mus musculus.

OS
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Sig_peptide 20..464
 FT Region /label= Mat_protein 20..140
 FT Region /label= Variable 141..464
 FT Region /label= Constant 50..54
 FT /label= CDR_H1 /note= "claim 9"
 FT 69..84
 FT /label= CDR_H2 /note= "claim 9"
 FT 118..128
 FT /label= CDR_H3 /note= "claim 9"

XX AU9859701-A.

XX

PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Akio S. Hideyuki H. Hiroko Y., Jun O., Kimihisa I;
 PI Masahiko O., Nobufusa S., Shin Y., Tohru T;
 XX
 DR WPI; 1998-543440/47.
 XX
 DR N-ESDB; V71029.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 FS Reference Example 4; Page 187-188; 292pp; English.

CC This is the amino acid of the heavy chain of murine anti-human Fas
 CC monoclonal antibody HFE7A. cDNA (see V70129) encoding the heavy
 CC chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
 CC RNA by RT-PCR (see V70125-26). The invention provides humanised
 CC HFE7A antibodies (see W83031-37) produced by CDR grafting. These
 CC antibodies are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. They are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to treat
 CC such diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX

SQ Sequence 464 AA;

Query Match 79.5%; Score 523; DB 19; Length 464;
 Best Local Similarity 83.5%; Pred. No. 1.4e-35;
 Matches 101; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSVKLSCKGCGYGTFTSYMMHWVKQRPQGGLWGEIDPSESNTNY 60
 DB 20 :||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 20 qvqlqpgaelvpgasvksckasgyftfswmhwkqrpqgglwgeidpsdsytny 79
 QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDYVYCARGYDGDYDAIDYWGQGTSTVTS 120
 DB 80 :||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
 80 ngkfkgtatltvdtsstaysmqlssltedsavyycarsdygshf--dywgqgttvtvs 139
 QY 121 \$ 121
 DB 140 s 140

RESULT 8

BL4747 ID BL4747 standard; Protein: 464 AA.

XX

AC BL4747;

XX

DT 24-NOV-2000 (first entry)

XX

DE Mouse anti-Fas antibody HFE7A heavy chain.

XX

KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;

QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYYCARGYDGDWDYADIDYWGQGTSTVTVS 120
 DB 80 NDKFKGKATLTVDSSSTAYMQLSSLTSEDSSAVYYCARNRYSNNWYFDWGTGTTVTVS 139
 QY 121 S 121
 DB 140 S 140

RESULT 10

ID R84555 standard; Protein; 122 AA.
 XX
 AC R84555;
 XX
 DT 02-FEB-1996 (first entry)
 XX
 DE B-cell lymphoma CH12 IgM heavy chain.
 XX
 KW Monoclonal antibody; Mab; SCH94.03; hybridoma; central nervous system;
 KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
 KW B-cell lymphoma; CH12; IgM.
 XX
 OS Mus sp.
 XX
 PN W09530004-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 27-APR-1995; 95WO-US05262.
 XX
 PR 29-APR-1994; 94US-0236520.
 XX
 PA (MAYO-) MAYO FOUNDATION.
 XX
 PI Miller DJ, Rodriguez M;
 XX
 WPI; 1995-393077/50.
 DR N-PSDB; T05314.
 XX
 XX Monoclonal antibodies which stimulate central nervous system
 PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
 PT treating multiple sclerosis, and viral or post-neural diseases of
 PT the CNS.
 XX
 PS Disclosure; Page 40; 63pp; English.
 CC
 CC The heavy chain variable region amino acid sequence (given
 CC in R84554) of monoclonal antibody SCH94.03 shows extensive sequence
 CC similarity with the corresp. sequence (R84555) of the IgM produced
 CC by B-cell lymphoma CH12.
 XX
 SQ Sequence 122 AA;

Query Match 79.1%; Score 520.5; DB 16; Length 122;
 Best Local Similarity 81.1%; Pred. No. 5.7e-36;
 Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLQPGAEELVKPCTSVKLSCKGYGFTSYWMHWKQRPQGGLEWIGEDIPSESNTNY 60
 DB 1 QVQLQPGTELVKPGASVKLSCKASGYFTSYWMHWKQRPQGGLEWIGNINPSNGGNTY 60
 QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYYCARGGY-DGWDYADIDYWGQGTSTVTV 119
 DB 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSSAVYYRDYDYGSSWGYFDYWGQGTTLTV 120
 QY 120 SS 121
 DB 121 SS 122

RESULT 11

R79861
 ID R79861 standard; Protein; 119 AA.
 XX
 AC R79861;
 XX
 DT 02-JUL-1996 (first entry)
 XX
 DE Anti-EGFR antibody heavy chain variable region (Clone L2 12B).
 XX
 KW Single chain antibody; antibody; epidermal growth factor receptor;
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
 KW assessment; phage antibody library.
 XX
 OS Mus musculus.
 XX
 PN W09525167-A1.
 XX
 PD 21-SEP-1995.
 XX
 PF 16-MAR-1995; 95WO-EP00978.
 XX
 PR 02-DEC-1994; 94EP-0118970.
 PR 17-MAR-1994; 94EP-0104160.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;
 PI Kettleborough AC, Mitjans F, Pluats J, Rosell E;
 XX
 WPI; 1995-336972/43.
 DR N-PSDB; T04014.
 XX
 PT Anti-EGFR antibodies and single chain Fv antibody fragments -
 PT obtained from phage-antibody libraries, useful for diagnosis and
 PT therapy of tumours
 XX
 PS Claim 4; Page 50; 93pp; English.
 CC
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies
 CC and antibodies constructed from anti-EGFR antibody fragments can be
 CC used for diagnosis of tumours and assessment of tumour growth in
 CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See T04011-T04026 and
 CC R79858-R79873)
 XX
 SQ Sequence 119 AA;

Query Match 79.0%; Score 520; DB 16; Length 119;
 Best Local Similarity 81.8%; Pred. No. 6.1e-36;
 Matches 99; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLQPGAEELVKPCTSVKLSCKGYGFTSYWMHWKQRPQGGLEWIGEDIPSESNTNY 60
 DB 1 QVQLQSGPELVKPGALVKLSCKASGYFTSYWMHWKQRPQGGLEWIGELDPSDSYTN 60
 QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYYCARGGYDGDWDYADIDYWGQGTSTVTVS 120
 DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSSAVYYCARSQSDYGSNHF--DYWGQGTTLTVS 118
 QY 121 S 121
 DB 119 S 119

RESULT 12

R76085
 ID R76085 standard; Peptide; 445 AA.
 XX

AC R76085;
 XX 21-NOV-1995 (first entry)
 XX MAB 55.1 heavy chain.
 XX
 XX Antigen binding structure; complementarity determining region; CDR;
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
 KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
 KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin.
 XX
 XX Mus sp.
 XX WO9515382-A.
 PN 08-JUN-1995.
 XX
 XX 29-NOV-1994; 94WO-GH02610.
 XX
 XX 03-JUN-1994; 94GB-0011089.
 PR 03-DEC-1993; 93GB-0024819.
 XX
 XX (ZENE) ZENECA LTD.
 PA
 XX Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
 PI Rose MS, Wright AF;
 XX WPI; 1995-215262/28.
 XX
 XX Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 XX Claim 3; Page 97-98; 121pp; English.
 XX
 XX An antigen binding structure is based on the CDRs (given in R76078-
 CC 84) of the heavy (R76085) and light (R76086) chains of MAB 55.1
 CC (ECACC 93081901), which recognises the colorectal tumor-associated
 CC antigen CA55.1. It is optionally humanized and in the form F(ab')₂,
 CC F(ab)', Fab, Fv, scFv or V-min, and is produced in transgenic
 CC animals or plants.
 XX
 XX Sequence 445 AA;
 SQ
 Query Match 79.0%; Score 520; DB 16; Length 445;
 Best Local Similarity 80.2%; Pred. No. 2.3e-35;
 Matches 97; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 QVQLQQPGAEIVKPGTSVKLSCKGSGYFTFTSYMMHWYKQRPQGGLWIGEDIPSESNTNY 60
 Db 1 qvqlqqpgaelvkgasvqlsckasgyftfgywlhwvkqrpqgglewignpstgrsdy 60
 QY 61 NQPKFGKATITVDISSSTAYWQLSSLTSEDSAVYYCARGYDGDWDYDAIDYWGQGTSTVTS 120
 Db 61 nekfkknkatitvdkssstaymqllssltseedsavyyccaraygyddamywgggtsvts 120
 QY 121 S 121
 Db 121 S 121
 RESULT 13
 R76088
 ID R76088 standard; Protein; 464 AA.
 XX AC R76088;
 XX
 XX 21-NOV-1995 (first entry)
 XX MAB 55.1 heavy chain.
 XX

KW Antigen binding structure; complementarity determining region; CDR;
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
 KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
 KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin.
 XX
 XX Mus sp.
 XX OS
 XX Key Location/Qualifiers
 FH 1..19
 FT Peptide /label= sig_peptide
 FT Protein 20..464
 FT /label= Mat_protein
 FT /note= "claim 3, page 97-98"
 XX
 XX WO9515382-A.
 PN 08-JUN-1995.
 XX
 XX 29-NOV-1994; 94WO-GH02610.
 XX
 XX 03-JUN-1994; 94GB-0011089.
 PR 03-DEC-1993; 93GB-0024819.
 XX
 XX (ZENE) ZENECA LTD.
 PA
 XX Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
 PI Rose MS, Wright AF;
 XX WPI; 1995-215262/28.
 DR N-PSDB; 094037.
 XX
 XX Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 XX Disclosure; Fig.15; 121pp; English.
 XX
 XX MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. cDNAs for the heavy (094037) and light (094036)
 CC chains of 55.1 were isolated, and F(ab)', F(ab')₂, Fab, Fv, scFv or
 CC V-min humanized 55.1 constructs have been expressed in myeloma
 CC cells and E. coli.
 XX
 XX Sequence 464 AA;
 SQ
 Query Match 79.0%; Score 520; DB 16; Length 464;
 Best Local Similarity 80.2%; Pred. No. 2.4e-35;
 Matches 97; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 QVQLQQPGAEIVKPGTSVKLSCKGSGYFTFTSYMMHWYKQRPQGGLWIGEDIPSESNTNY 60
 Db 20 qvqlqqpgaelvkgasvqlsckasgyftfgywlhwvkqrpqgglewignpstgrsdy 79
 QY 61 NQPKFGKATITVDISSSTAYWQLSSLTSEDSAVYYCARGYDGDWDYDAIDYWGQGTSTVTS 120
 Db 80 nekfkknkatitvdkssstaymqllssltseedsavyyccaraygyddamywgggtsvts 139
 QY 121 S 121
 Db 140 S 140
 RESULT 14
 W27122
 ID W27122 standard; Protein; 118 AA.
 XX AC W27122;
 XX
 XX 04-JAN-1998 (first entry)
 XX Murine antibody heavy chain variable region consensus.
 DE


```

XX Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
KW human milk fat globule; HMF; tumour; Breast cancer; vaccine.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
XX Region 31..35
XX /label= CDR1
XX /note= "complementarity determining region 1"
XX Region 50..66
XX /label= CDR2
XX /note= "complementarity determining region 2"
XX Region 99..107
XX /label= CDR3
XX /note= "complementarity determining region 3"
XX Misc-difference 100
XX /note= "unspecified amino acid residue"
XX Misc-difference 101
XX /note= "unspecified amino acid residue"
XX Misc-difference 102
XX /note= "unspecified amino acid residue"
XX
XX WO9722699-A2.
XX
XX 26-JUN-1997. 96WO-US20757.
XX
XX 19-DEC-1996; 96WO-US20757.
XX
XX 13-DEC-1996; 96US-0575762.
XX 20-DEC-1995; 95US-0575762.
XX 26-JAN-1996; 96US-0591965.
XX
XX (KENT ) UNIV KENTUCKY.
XX
XX Chatterjee M, Chatterjee SK, Foon KA;
XX WPI; 1997-341690/31.
XX
XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
XX against human milk fat globule disease associated tumours,
XX especially breast cancer
XX
XX Example 2; Fig 26C; 130pp; English.
XX
XX This polypeptide sequence comprises a consensus sequence of murine
XX heavy chain variable regions (VH) selected on the basis of identity
XX to the VH region (see W27120) of monoclonal anti-idiotypic antibody
XX 11D10. The sequences were obtained from a GenBank database
XX search. A VL consensus (W27121) was also produced. 11D10 has at
XX least 18 departures from the consensus sequences (7 in the light
XX chain and 11 in the heavy chain). 8 occur within CDRs and 10
XX outside CDRs. 11D10 polypeptides and polynucleotides can be
XX used in vaccines and pharmaceutical compositions for the treatment
XX of human milk fat globule-associated diseases such as breast
XX cancer.
XX
XX Sequence 118 AA;
XX
XX
XX Query Match 78.8%; Score 518.5; DB 18; Length 118;
XX Best Local Similarity 81.8%; Pred. No. 8e-36;
XX Matches 99; Conservative 5; Mismatches 14; Indels 3; Gaps 1;
XX
XX 1 QVQLQPGAEVLKPGTSTKLSCKGTYFTSYWVHWVQKRPQGGLEWIGEDPSNTNY 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 qvqlqsgaelvrpgasvmsckasgyftsywvhwvkwkrrpgdgglewlgaypgngdtny 60
XX
XX 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYVCARGYDCWDVAIDYWGOGTSVTVS 120
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 61 nqkfkakatltadtssstaysmqllssltseedsavvfcarxxxg---amdywgqgtsvtvs 117
XX
XX 121 S 121

```

```

Db 118 s 118
RESULT 15
R54756
ID R54756 standard; Protein; 269 AA.
XX
XX AC R54756;
XX
XX DT 06-DEC-1994 (first entry)
XX
XX DE PRAS111 between HindIII and EcoRI sites.
XX
XX KW Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus;
XX Penton fibre; Ad5; Fusion sites; PCR; polymerase chain reaction.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Protein 1..269
XX FT /label= Single chain Fv fragment
XX FT Peptide 1..22
XX FT /label= pelB leader peptide
XX FT Protein 23..142
XX FT /label= heavy chain variable region
XX FT Region 23..51
XX FT /label= VH FR1
XX FT Region 52..57
XX FT /label= VH CDR 1
XX FT Region 58..71
XX FT /label= VH FR2
XX FT Region 72..86
XX FT /label= VH CDR 2
XX FT Region 89..120
XX FT /label= VH FR3
XX FT Region 121..131
XX FT /label= VH CDR 3
XX FT Region 132..142
XX FT /label= VH FR4
XX FT Peptide 143..265
XX FT /label= (G4S)3 Linker
XX FT Protein 158..269
XX FT /label= Light chain variable region
XX FT Region 158..179
XX FT /label= VL FR1
XX FT Region 180..193
XX FT /label= VL CDR 1
XX FT Region 194..207
XX FT /label= VL FR2
XX FT Region 208..215
XX FT /label= VL CDR 2
XX FT Region 216..247
XX FT /label= VL FR3
XX FT Region 248..256
XX FT /label= VL CDR 3
XX FT Region 257..269
XX FT /label= VL FR3
XX
XX WO9410323-A.
XX
XX 11-MAY-1994.
XX
XX 04-NOV-1993; 93WO-CB02267.
XX
XX 04-NOV-1992; 92GB-0023084.
XX
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
XX Epenetos AA, Spooner RA;
XX WPI; 1994-167477/20.
XX
XX N-PSDB; Q64817.

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:35:04 ; Search time 4.45 seconds
(without alignments)
47.200 Million cell updates/sec

Title: US-08-700-737-9
Perfect score: 658
Sequence: 1 QVQLQPGAEILVKPGTSVKL.....DGWDYADYWGQTSVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7695 seqs, 1735856 residues

Total number of hits satisfying chosen parameters: 7695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	73.9	140	4	US-08-475-815A-11
2	426	64.7	132	5	US-09-386-658-2
3	278.5	42.3	482	5	US-09-509-031-16
4	242	36.8	240	5	US-09-782-504-4
5	107	16.3	155	5	US-09-509-031-11
6	107	16.3	342	5	US-09-509-031-6
7	107	16.3	495	5	US-09-509-031-4
8	105	16.0	128	4	US-08-475-815A-7
9	69.5	10.6	442	5	US-09-739-449-9534
10	65.5	10.0	914	5	US-09-193-562D-28
11	65	9.9	753	1	PCT-US01-09226-51
12	64	9.7	281	5	US-09-739-449-11638
13	62.5	9.5	109	5	US-09-386-658-4
14	62.5	9.5	170	5	US-09-814-950-4
15	62.5	9.5	172	5	US-09-814-950-2
16	62	9.4	517	5	US-09-739-449-12328
17	60.5	9.2	1008	5	US-09-308-453-2
18	60	9.1	757	5	US-09-739-449-11939
19	59.5	9.0	639	5	US-09-739-449-11223
20	59	9.0	574	5	US-09-815-108-7
21	58.5	8.9	342	5	US-09-815-108-20
22	58.5	8.9	379	5	US-09-813-408-6
23	58.5	8.9	448	5	US-09-815-108-6
24	58.5	8.9	472	5	US-09-815-108-5
25	58.5	8.9	504	5	US-09-815-108-8
26	58.5	8.9	504	5	US-09-815-108-15
27	58.5	8.9	504	5	US-09-815-108-17

28	58.5	8.9	504	5	US-09-815-108-19
29	58.5	8.9	509	5	US-09-815-108-3
30	58.5	8.9	529	5	US-09-815-108-2
31	58.5	8.9	594	5	US-09-815-108-22
32	57	8.7	251	5	US-09-739-449-12898
33	56	8.5	652	5	US-09-813-742-5
34	56	8.5	1144	5	US-09-813-742-3
35	55.5	8.4	571	5	US-09-809-391-481
36	55	8.4	101	5	US-09-809-391-754
37	55	8.4	215	5	US-09-739-449-10936
38	55	8.4	216	5	US-09-739-449-12644
39	55	8.4	238	5	US-09-809-391-485
40	54.5	8.3	178	5	US-09-509-031-13
41	54.5	8.3	198	5	US-09-509-031-8
42	54.5	8.3	358	5	US-09-739-449-11717
43	54	8.2	299	5	US-09-739-449-9917
44	54	8.2	1758	5	US-09-739-449-11627
45	53.5	8.1	249	5	US-09-739-449-8182

ALIGNMENTS

RESULT 1
US-08-475-815A-11
; Sequence 11, Application US/08475815A
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIO LABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-815A-11

Sequence 19, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 22, Appl
Sequence 12898, A
Sequence 5, Appl
Sequence 3, Appl
Sequence 481, App
Sequence 754, App
Sequence 10936, A
Sequence 12644, A
Sequence 485, App
Sequence 13, Appl
Sequence 8, Appl
Sequence 11717, A
Sequence 9917, Ap
Sequence 11627, A
Sequence 8182, Ap

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cmMLgI protein
; OTHER INFORMATION: sequence
US-09-509-031-16

Query Match      42.3%; Score 278.5; DB 5; Length 482;
Best Local Similarity 43.9%; Pred. No. 1.9e-22;
Matches 54; Conservative 27; Mismatches 39; Indels 3; Gaps 2;

QY 1 QVLOQPGAELVKPGTQSVKLSCKGCGYFTFTSYMMHWVKQRPQGQLEWI--GEIDPSESNT 58
Db 20 QVLOQPGAELVKPGASVKMSCKASGYFTFTSYMMHWKQTPGRLGLEWIGAIYPGNGDTSY 79
QY 61 NQKFKGKATLTVDISSTAYMQLSLTSDSAVYVCARGGYDWDYADYWGQGTSTVTS 120
Db 80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYVCARSTYGGWYFNVWGAGTTVTS 139
QY 121 S 121
Db 140 A 140

RESULT 2
US-09-386-658-2
; Sequence 2, Application US/09386658
; GENERAL INFORMATION:
; APPLICANT: Erlanger, Bernard
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
; FILE REFERENCE: 0575-54182/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/386,658
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: mouse [murine]
US-09-386-658-2

Query Match      64.7%; Score 426; DB 5; Length 132;
Best Local Similarity 67.8%; Pred. No. 2.6e-38;
Matches 82; Conservative 10; Mismatches 21; Indels 8; Gaps 1;

QY 1 QVLOQPGAELVKPGTQSVKLSCKGCGYFTFTSYMMHWVKQRPQGQLEWIGIDPSESNTNY 60
Db 20 QVHLQSGPELVPRGASVKISKTSIGYVFSSWMWVKQRPQGQKWKIGRIYPCNGNTNY 79
QY 61 NQKFKGKATLTVDISSTAYMQLSLTSDSAVYVCARGGYDWDYADYWGQGTSTVTS 120
Db 80 NEKFKGKATLTADKSSNTAYMQLSLTSDSAVYFCATSS-----AYWGQGTLLTVS 131
QY 121 S 121
Db 132 A 132

RESULT 3
US-09-509-031-16
; Sequence 16, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cmMLgI protein
; OTHER INFORMATION: sequence
US-09-509-031-16

Query Match      42.3%; Score 278.5; DB 5; Length 482;
Best Local Similarity 43.9%; Pred. No. 1.9e-22;
Matches 54; Conservative 27; Mismatches 39; Indels 3; Gaps 2;

QY 1 QVLOQPGAELVKPGTQSVKLSCKGCGYFTFTSYMMHWVKQRPQGQLEWI--GEIDPSESNT 58
Db 31 EVKLIVESGGLVOPGGSLRLSCATSGTFFSDFYEWYRQPPGKLEWIAASRNKNGKYYT 90
QY 59 NYNQKFKGKATLTVDISSTAYMQLSLTSDSAVYVCARGGYDWDYADYWGQGTSTVTS 118
Db 91 EYSASVKGRFIVSRDTSQSIILYLMNALRAEDTAIYYCAR--NYYGSTWCFDVGAGTTVT 149
QY 119 VSS 121
Db 150 VSS 152

RESULT 4
US-09-782-504-4
; Sequence 4, Application US/09782504
; GENERAL INFORMATION:
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; APPLICANT: Bruce, Kim Folger
; APPLICANT: Schreiber, George J.
; APPLICANT: Siegall, Clay
; APPLICANT: McAndrew, Stephen
; TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN CARCINOMAS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,504
; FILING DATE: 12-Feb-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 840065.405D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-782-504-4

Query Match      36.8%; Score 242; DB 5; Length 240;
Best Local Similarity 47.9%; Pred. No. 4.8e-19;
Matches 58; Conservative 24; Mismatches 31; Indels 8; Gaps 7;
```



```

Query Match          16.0%; Score 105; DB 4; Length 128;
Best Local Similarity 27.0%; Pred. No. 3e-05;
Matches 33; Conservative 23; Mismatches 46; Indels 20; Gaps 7;

QY      1 QVLOQPAGFL-VKPGTSVKLSCKGYGYFTSYWMHWKORPQGLE-WIGEIDPSESNT 58
Db      1 : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      23 QIVLSGSPAILASPEKYMTTCRA---SSVSYSIHWFQKPGSPKPMI--YATSNLAS 77
Db      23 : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      59 NYNQKFKGKATLIVDISSTAY-MQLSSLTISDSAVYYCARGYDGDWDAIDYWGOGTSV 117
Db      59 : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      78 GVPVRESG-----GSGTYSLTISRVEADAATYYCQ-----WTSNPPTFGGGTKL 125
Db      78 : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      118 TV 119
Db      126 EI 127

RESULT          9
US-09-739-449-9534
; Sequence 9534, Application US/09739449
; GENERAL INFORMATION: Gregory J.
; APPLICANT: Hinkle, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9534

```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 753
; TYPE: PRF
; ORGANISM: Homo sapiens
PCT-US01-09226-51

```

```

Query Match          9.98; Score 65; DB 1; Length 753;
Best Local Similarity 24.78; Pred. No. 3.1;
Matches 21; Conservative 15; Mismatches 33; Indels 16; Gaps 3;

Qy 1 QVQLQQPAAELVKPGT-----SVKLSCKGCGYFTFSYMHHWKQRPQGLEWIGEI 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 RVEIQRAG---ENGTCDDDFTLQAAILLCRELGFTFATGWTSAKYGPGTGRIWLDNL 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 52 DPS---ESNTNYNQKFKGKATLTVD 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 SCSTEQSVTECASRGWGNSDCTHD 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 12
US-09-739-449-11638
; Sequence 11638, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(13490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 11638
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11638

```

```

Query Match      9.7%: Score 64; DB 5; Length 281;
Best Local Similarity 25.8%; pred. No. 1.3;
Matches 23; Conservative 17; Mismatches 35; Indels 14; Gaps 4;

QY      24  GYCYTTSTVMHWVKORPQGLEIGEDIPSESNTNTNORFKGKATLTVDISSTAYMOL 83
      | | | | : | | | | | : | | : | | : | | : | | : | | : | | :
Db      90  GVGYQENNYF-----RSDVTLDYMGKSRDFRGSTGFCGSPGRC--VSADLSLSAYTILM 142

QY      84  SS-----LTSEDSAVYYCA---RGYDGDWD 105
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     143  ANAYVDLGLTYGSIITPYVGGGIGGSGVVKWD 171

```

```

RESULT 13
US-09-386-658-4
; Sequence 4, Application US/09386658
; GENERAL INFORMATION:
; APPLICANT: Erlanger, Bernard
; APPLICANT: Chen, Bi-Xing
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
; FILE REFERENCE: 0575-54182/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/386,658
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-09-386-658-4

```

US-09-386-658-4

Query Match	9.5%;	Score 62.5;	DB 5;	Length 109;
Best Local Similarity	23.2%;	Pred. No. 0.6;		
Matches 29;	Conservative 20;	Mismatches 49;	Indels 27;	Gaps 9;
QY	2	VQLQOPGAEL-VKPGTSVKLSCKGCGYTTSTVMHWKQRPQGLEWTGEID-----PSE	55	
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	2	IOWTQTTSSLASLGRDVTFCSA-SQDINNY-LNMYQKPD-----GTTKLLIYYTSS	53	
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
QY	56	STNTYNQKEKGKATLTVDISSTAY-MOLSSITSEDSAVYYCARGYDGDWYADYWGQG	114	
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	54	LRSQVPSRFGS-----GSGTDYSLTNLPEEDIATYFCQQ--YSRLPFT---FGSG	101	
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
QY	115	TSVTV	119	
	:	:	:	:
	:	:	:	:
Db	102	TKLEI	106	

```

RESULT 14
US-09-814-950-4
; Sequence 4, Application US/09814950
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001174
; CURRENT APPLICATION NUMBER: US/09/814,950
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Human
US-09-814-950-4

```

```
Query Match          9.5%; Score 62.5; DB 5; Length 170;  
Best Local Similarity 21.3%; Pred. NO. 1;  
Matches 20; Conservative 9; Mismatches 36; Indels 29; Gaps 1;  
  
Qy      3 QLOPGAEILVPGTSVKUSCKGYGVTFTSYMMHWYKQRFGGLEWIGETIDPSESNTNYNQ 62  
         | : | | | : | : | : | : | : |  
Db      62 QISOPEYVAAPGESLEVRCLLKAAAVISWTKDGVHLGNPNRTVLIGE----- 109  
  
Qy      63 KFKKGATLTVDISSSTAYMOLSSLTSEDSVAYYC 96  
         | : | : | : | : | : | : | : |  
Db     110 -----YLQIKGATPRDSGLIAC 126
```

```

RESULT 15
US-09-814-950-2
; Sequence 2, Application US/09814950
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001174
; CURRENT APPLICATION NUMBER: US/09/814,950
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human
US-09-814-950-2

```

Query Match 9.5%; Score 62.5; DB 5; Length 172;
Best Local Similarity 21.3%; Pred. No. 1;
Matches 20; Conservative 9; Mismatches 36; Indels 29; Gaps 1;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2001, 17:35:03 ; Search time 117.03 Seconds
(without alignments)
166.311 Million cell updates/sec

Title: US-08-700-737-9
Perfect score: 658
Sequence: 1 QVQLQPGAEELVKGTSVKL.....DGWDYADYWGQGTSTVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main.*

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- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pcp.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pcp.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pcp.*
- 23: /cgn2_6/ptodata/2/paa/US060_COMB.pcp.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	100.0	121	11	US-08-700-737-9
2	658	100.0	140	11	US-08-700-737-15
3	658	100.0	144	11	US-08-700-737-2
4	646	98.2	137	11	US-08-700-737-4
5	572	86.9	121	11	US-08-700-737-55
6	572	86.9	180	11	US-08-700-737-19
7	536	81.5	119	9	US-08-073-967-44
8	536	81.5	119	9	US-08-553-497-12
9	525	79.8	127	11	US-08-700-737-53
10	524	79.6	119	8	US-08-443-540-62

11	523	79.5	464	14	US-09-053-583-9	Sequence 9, Appl
12	523	79.5	464	18	US-09-408-646-9	Sequence 9, Appl
13	523	79.5	464	18	US-09-499-662-9	Sequence 9, Appl
14	520.5	79.1	122	10	US-08-592-084-28	Sequence 28, Appl
15	520.5	79.1	122	11	US-08-779-784-28	Sequence 28, Appl
16	520.5	79.1	122	17	US-09-322-862-28	Sequence 28, Appl
17	520	79.0	119	9	US-08-553-497-8	Sequence 8, Appl
18	518.5	78.8	118	11	US-08-766-350A-48	Sequence 48, Appl
19	518.5	78.8	118	12	US-08-836-455-48	Sequence 48, Appl
20	518.5	78.8	118	12	US-08-836-455-48	Sequence 48, Appl
21	517.5	78.6	269	15	US-09-120-809-72	Sequence 72, Appl
22	517.5	78.6	269	17	US-09-313-928-3	Sequence 3, Appl
23	517.5	78.6	402	17	US-09-313-928-9	Sequence 3, Appl
24	517.5	78.6	415	17	US-09-313-928-7	Sequence 7, Appl
25	517.5	78.6	435	17	US-09-313-928-5	Sequence 5, Appl
26	517	78.6	119	8	US-08-443-540-61	Sequence 61, Appl
27	516.5	78.5	120	4	US-08-024-712-6	Sequence 6, Appl
28	515	78.4	119	8	US-08-443-540-63	Sequence 63, Appl
29	513.5	78.0	120	3	US-07-881-109-21	Sequence 21, Appl
30	513.5	78.0	120	3	US-07-881-109A-21	Sequence 21, Appl
31	513.5	78.0	120	7	US-08-313-198-21	Sequence 21, Appl
32	513.5	78.0	120	11	US-08-720-323-21	Sequence 21, Appl
33	513	78.0	119	8	US-08-443-540-60	Sequence 60, Appl
34	513	78.0	119	8	US-08-462-798-6	Sequence 6, Appl
35	513	78.0	119	9	US-08-541-373-6	Sequence 6, Appl
36	513	78.0	119	9	US-08-541-373A-6	Sequence 6, Appl
37	508	77.2	140	8	US-08-487-165-24	Sequence 24, Appl
38	507	77.1	117	15	US-09-157-370-2	Sequence 2, Appl
39	505	76.7	119	18	US-09-406-532-2	Sequence 2, Appl
40	502.5	76.4	240	15	US-09-159-027-4	Sequence 4, Appl
41	502.5	76.4	241	3	US-07-828-832-11	Sequence 11, Appl
42	502.5	76.4	241	8	US-08-465-473A-11	Sequence 11, Appl
43	502.5	76.4	637	3	US-07-828-832-16	Sequence 16, Appl
44	502.5	76.4	637	8	US-08-465-473A-16	Sequence 16, Appl
45	501	76.1	111	8	US-08-443-540-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-700-737-9
; Sequence 9, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; TITLE OF INVENTION: INTEGRIN
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10

us-08-700-737-9.rapm

Sat Apr 14 08:10:28 2001

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-700-737-9

Query Match      100.0%; Score 658; DB 11; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.2e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
Db 1 QVQLQPGAEELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
Db 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 2
US-08-700-737-15
; Sequence 15, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-700-737-15
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-700-737-9

Query Match      100.0%; Score 658; DB 11; Length 140;
Best Local Similarity 100.0%; Pred. No. 8.6e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
Db 20 QVQLQPGAEELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 79
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
Db 80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 139
QY 121 S 121
Db 140 S 140

RESULT 3
US-08-700-737-2
; Sequence 2, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-700-737-2

Query Match      100.0%; Score 658; DB 11; Length 144;
Best Local Similarity 100.0%; Pred. No. 8.8e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
Db 20 QVQLQPGAEELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 79
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
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100

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Sat Apr 14 08:10:28 2001

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; ZIP: 02173
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-700-737-19

Query Match 86.9%; Score 572; DB 11; Length 180;
Best Local Similarity 86.0%; Pred. No. 4.le-49;
Matches 104; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVLKPGTQSVKLSCKGCGYTTFTSYMMHWVKORPGGLEWIGEIDPSESNTNY 60
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Db 20 QVQLVSGGAEVKKPGASVKVSKGSGYTTFTSYMMHWVRAQPGORLEWIGEIDPSESNTNY 79
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QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARGYDGDWDYDAIDYWGQGTSTVTS 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 NQKFKGRVTLTVDISASTAYMELSLRSEDTAVYICARGYDGDWDYDAIDYWGQGLTVTVS 139
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QY 121 S 121
    |
Db 140 S 140
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RESULT 7
US-08-073-967-44
; Sequence 44, Application US/08073967
; GENERAL INFORMATION:
; APPLICANT: Syamal K. Data
; TITLE OF INVENTION: METHODS FOR INHIBITING THE
; TITLE OF INVENTION: ACTIVITY OF PATHOGENIC T
; TITLE OF INVENTION: HELPER CELLS ASSOCIATED WITH
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,967
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US/07/764,686
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark

```

```

;
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00398/050001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-073-967-44

Query Match 81.5%; Score 536; DB 4; Length 119;
Best Local Similarity 84.3%; Pred. No. 9.7e-46;
Matches 102; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQPGAEVLKPGTQSVKLSCKGCGYTTFTSYMMHWVKORPGGLEWIGEIDPSESNTNY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLQPGAEVLKPGASVKLSCKASGYTTFTSYMMHWVKRPGQGLEWIGELNPSNGRTNY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARGYDGDWDYDAIDYWGQGTSTVTS 120
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Db 61 NQKFKRATLTVDKSSSTAYMQLSSLTSEDSAVYICARSG--GFYGMGYWGQGTSTVTS 118
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 S 121
    |
Db 119 S 119
    |

RESULT 8
US-08-553-497-12
; Sequence 12, Application US/08553497
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-EGFR Single-Chain Fvs and Anti-EGFR
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 32
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497-12

Query Match 81.5%; Score 536; DB 9; Length 119;
Best Local Similarity 85.1%; Pred. No. 9.7e-46;
Matches 103; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQPGAEVLKPGTQSVKLSCKGCGYTTFTSYMMHWVKORPGGLEWIGEIDPSESNTNY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLQSGAEVLKPGASVKLSCKASGYTTFTSYMMHWVKORPGQGLEWIGELDPSDYTN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARGYDGDWDYDAIDYWGQGTSTVTS 120
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Db 61 NQKFKRATLTVDKSSSTAYMQLSSLTSEDSAVYICARSDYGSSEHF--DYWGQGTTVTVS 118
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QY 121 S 121
    |
Db 119 S 119
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```



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RESULT 14
US-08-692-084-28
; Sequence 28, Application US/08692084
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/692,084
; FILING DATE: 08-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-692-084-28

Query Match 79.1%; Score 520.5; DB 10; Length 122;
Best Local Similarity 81.1%; Pred. No. 3.5e-44;
Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

Qy 1 QVQLQQPQGAELVKPGTQSVKLSCKGKGYGTFSTSYNMHWKQRPQGLEWIGEDPSESNTNY 60
Db 1 QVQLQQPQGTETLVKPGASVKLSCKASGYTFSTSYNMHWKQRPQGLEWIGNINPSNGGTNY 60
Qy 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYDAIDYWGQGTSTVTV 119
Db 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYARDYGYSSWGYYFDYWGQGTTLTV 120
Qy 120 SS 121
Db 121 SS 122

RESULT 15

US-08-779-784-28
; Sequence 28, Application US/08779784
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-784-28

Query Match 79.1%; Score 520.5; DB 11; Length 122;
Best Local Similarity 81.1%; Pred. No. 3.5e-44;
Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

Qy 1 QVQLQQPQGAELVKPGTQSVKLSCKGKGYGTFSTSYNMHWKQRPQGLEWIGEDPSESNTNY 60
Db 1 QVQLQQPQGTETLVKPGASVKLSCKASGYTFSTSYNMHWKQRPQGLEWIGNINPSNGGTNY 60
Qy 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYDAIDYWGQGTSTVTV 119
Db 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYARDYGYSSWGYYFDYWGQGTTLTV 120
Qy 120 SS 121
Db 121 SS 122

Search completed: April 13, 2001, 17:37:47
Job time: 164 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:34:02 ; Search time 28.17 Seconds
(without alignments)
82.517 Million cell updates/sec

Title: US-08-700-737-9
Perfect score: 658
Sequence: 1 QVQLQQPGAEIVKPTSVKL.....DGWDVAIDYWGQTSVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Query Match	Score	Length	DB ID	Description
1	536	81.5	119	2	US-08-553-497A-12
2	524	79.6	119	3	US-08-881-037-62
3	520.5	79.1	122	1	US-08-236-520-9
4	520.5	79.1	122	5	PCT-US95-05262-9
5	520	79.0	119	2	US-08-533-497A-8
6	520	79.0	445	1	US-08-353-400-33
7	520	79.0	464	1	US-08-428-257A-72
8	517.5	78.6	269	2	US-08-491-988-3
9	517.5	78.6	402	2	US-08-491-988-9
10	517.5	78.6	415	2	US-08-491-988-5
11	517.5	78.6	435	2	US-08-881-037-61
12	517.5	78.6	419	3	US-08-881-037-63
13	517	78.4	119	3	US-08-881-037-60
14	513	78.0	119	3	US-08-881-037-60
15	513	78.0	119	3	US-08-881-037-60
16	513	78.0	119	3	US-08-881-037-60
17	508	77.2	140	1	US-07-946-421-24
18	502.5	76.4	241	1	US-08-235-838-11
19	502.5	76.4	241	1	US-08-235-838-11
20	502.5	76.4	241	1	US-08-235-838-11
21	502.5	76.4	241	1	US-08-235-838-11
22	501	76.1	637	2	US-08-465-473B-16
23	500	76.0	244	2	US-08-881-037-14
24	500	76.0	244	2	US-08-881-037-14
25	498	75.7	116	2	US-08-553-497A-20
26	496	75.4	143	1	US-08-737-560A-7
27	496	75.4	143	5	PCT-US95-05262-7

28	495	75.2	139	2	US-08-894-922A-5	Sequence 5, Appl
29	495	75.2	252	2	US-08-894-922A-14	Sequence 14, Appl
30	495	75.2	271	2	US-08-894-922A-10	Sequence 10, Appl
31	494	75.1	111	3	US-08-881-037-16	Sequence 16, Appl
32	494	75.1	118	3	US-09-065-059-5	Sequence 5, Appl
33	494	75.1	119	2	US-08-737-560A-10	Sequence 10, Appl
34	494	75.1	136	5	PCT-US93-11611-4	Sequence 4, Appl
35	494	75.1	244	2	US-08-553-497A-22	Sequence 22, Appl
36	493.5	75.0	120	1	US-08-211-202-1	Sequence 1, Appl
37	493.5	75.0	246	1	US-08-469-486-57	Sequence 57, Appl
38	493.5	75.0	246	2	US-08-469-486-57	Sequence 57, Appl
39	493	74.9	111	3	US-08-881-037-17	Sequence 17, Appl
40	493	74.9	242	2	US-08-553-497A-26	Sequence 26, Appl
41	490	74.5	111	3	US-08-881-037-15	Sequence 15, Appl
42	489	74.3	138	1	US-08-482-882-78	Sequence 78, Appl
43	489	74.3	138	2	US-08-483-389-78	Sequence 78, Appl
44	489	74.3	138	2	US-08-487-113D-78	Sequence 78, Appl
45	489	74.3	138	3	US-08-714-017-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1
US-08-553-497A-12
; Sequence 12, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLERBROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAM, JAUME
; APPLICANT: MITJANS, FRANCES
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553.497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 12:

Query Match 79.6%; Score 524; DB 3; Length 119;
Best Local Similarity 83.7%; Pred. No. 4.2e-41;

RESULT 4
 PCT-US95-05262-9
 : Sequence 9, Application PC/TUS9505262
 : GENERAL INFORMATION:
 : APPLICANT: Mayo Foundation for Medical Education Research
 : TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
 : TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
 : STREET: Two Militia Drive
 : CITY: Lexington
 : STATE: Massachusetts
 : COUNTRY: USA
 : ZIP: 02173
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US95/05262
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: U.S. 08/236,520
 : FILING DATE: April 29, 1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Granahan, Patricia
 : REGISTRATION NUMBER: 27,227
 : REFERENCE/DOCKET NUMBER: MMV92-01 PCT
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-861-6240
 : TELEFAX: 617-861-9540
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 122 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : PCT-US95-05262-9

Query Match 79.1%; Score 520.5; DB 5; Length 122;
 Best Local Similarity 81.1%; Pred. No. 9e-41;
 Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;
 QY 1 QVLOQPQGAELVKPGTSVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
 Db 1 QVLOQPQGTLYKPGASVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGINPNSGGTNY 60
 QY 61 NQKFKGKATLVDISSTAYMQLSLTSDSAVYYCARGGY-DGWDYDAIDYWGOGTSTVY 119
 Db 61 NEKFKSKATLVTKSSSTAYMQLSLTSDSAVYYCARGGY-DGWDYDAIDYWGOGTSTVY 119
 QY 120 SS 121
 Db 121 SS 122

RESULT 5
 US-08-553-497A-8
 : Sequence 8, Application US/08553497A
 : Patent No. 5844093
 : GENERAL INFORMATION:
 : APPLICANT: KETTLEBOROUGH, C. A.
 : APPLICANT: BENDIG, MARY M.
 : APPLICANT: ANSELL, KEITH H.
 : APPLICANT: GUSLOW, DETLEF
 : APPLICANT: ADAM, JAUME
 : APPLICANT: MITJANS, FRANCESCA
 : APPLICANT: ROSELL, ELISABET

: APPLICANT: BLASCO, FRANCESC
 : APPLICANT: PIULATS, JAUME
 : TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
 : TITLE OF INVENTION: ANTIBODIES
 : NUMBER OF SEQUENCES: 30
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
 : STREET: 2200 CLARENDON BLVD. SUITE 1400
 : CITY: ARLINGTON
 : STATE: VA
 : COUNTRY: US
 : ZIP: 22201
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/553.497A
 : FILING DATE: 17-NOV-1995
 : CLASSIFICATION: 530
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: WO PCT/EP95/00978
 : FILING DATE: 16-MAR-1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: EP 94104160.0
 : FILING DATE: 17-MAR-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: EP 94118970.6
 : FILING DATE: 02-DEC-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: HAMLET-KING, DIANA
 : REGISTRATION NUMBER: 33,302
 : REFERENCE/DOCKET NUMBER: MERCK 1726
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 703-243-6333
 : TELEFAX: 703-243-6410
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 119 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-553-497A-8

Query Match 79.0%; Score 520; DB 2; Length 119;
 Best Local Similarity 81.8%; Pred. No. 9.8e-41;
 Matches 99; Conservative 6; Mismatches 14; Indels 2; Gaps 1;
 QY 1 QVLOQPQGAELVKPGTSVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
 Db 1 QVLOQESGPELVKPGALVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
 QY 61 NQKFKGKATLVDISSTAYMQLSLTSDSAVYYCARGGYDGDYDAIDYWGOGTSTVYS 120
 Db 61 NQKFKGKATLVTKSSNTAYMQLSLTSDSAVYYCARGGYDGDYDAIDYWGOGTSTVYS 118
 QY 121 S 121
 Db 119 S 119

RESULT 6
 US-08-353-400-33
 : Sequence 33, Application US/08353400
 : Patent No. 5665357
 : GENERAL INFORMATION:
 : APPLICANT:
 : TITLE OF INVENTION: PROTEINS
 : NUMBER OF SEQUENCES: 37
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-33

Query Match 79.0%; Score 520; DB 1; Length 445;
Best Local Similarity 80.2%; Pred. No. 4.3e-40;
Matches 97; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
QY 1 QVQLQQPGAEIVKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGQLEWIGIDPSESNTNY 60
DB 1 QVQLQQPGAEIVKPGASVOLSKASGYTFTGYIHWKQRPQGQLEWIGVNPSTGRSDY 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYVCARGYDGDWDYDAIDYWGQGTSTVTS 120
DB 61 NEKFKNKATLTVDKSSSTAYMQLSSLTSEDSAVYVCARERAYGYDDAMDYWGQGTSTVTS 120
QY 121 S 121
DB 121 S 121

RESULT 7
US-08-353-400-36
Sequence 36, Application US/08353400
Patent No. 566:357
GENERAL INFORMATION:
APPLICANT: PROTEINS
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-36

Query Match 79.0%; Score 520; DB 1; Length 464;
Best Local Similarity 80.2%; Pred. No. 4.5e-40;
Matches 97; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
QY 1 QVQLQQPGAEIVKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGQLEWIGIDPSESNTNY 60
DB 20 QVQLQQPGAEIVKPGASVOLSKASGYTFTGYIHWKQRPQGQLEWIGVNPSTGRSDY 79
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYVCARGYDGDWDYDAIDYWGQGTSTVTS 120
DB 80 NEKFKNKATLTVDKSSSTAYMQLSSLTSEDSAVYVCARERAYGYDDAMDYWGQGTSTVTS 139
QY 121 S 121
DB 140 S 140

RESULT 8
US-08-428-257A-72
Sequence 72, Application US/08428257A
Patent No. 5885808
GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-72

Query Match 78.6%; Score 517.5; DB 2; Length 269;
Best Local Similarity 81.8%; Pred. No. 4.1e-40;
Matches 99; Conservative 4; Mismatches 17; Indels 1; Gaps 1;
QY 1 QVQLQQPGAEIVKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGQLEWIGIDPSESNTNY 60
DB 23 QVQLQQPGAEIVKPGASVOLSKASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSGGTKY 82
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYVCARGYDGDWDYDAIDYWGQGTSTVTS 120
DB 83 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYVCARYDYGYSSY-FDYWGQGTSTVTS 141
QY 121 S 121
DB 142 S 142
RESULT 9
US-08-491-988-3
Sequence 3, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:36:46 ; Search time 32.39 Seconds
(without alignments)

280.069 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPYTGGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	89.2	132	B25912	Ig kappa chain pre
2	576	82.9	113	H30560	Ig kappa chain v r
3	574	82.6	113	E30560	Ig kappa chain v r
4	563	81.0	112	S37203	Ig kappa chain v r
5	560.5	80.6	131	S39276	Ig kappa chain pre
6	553.5	79.6	131	B34904	Ig kappa chain pre
7	549.5	79.1	131	C34904	Ig kappa chain pre
8	548.5	78.9	114	PL0202	Ig kappa chain pre
9	546.5	78.6	131	B32513	anti-DNA autoantib
10	546.5	78.6	131	B30577	Ig kappa chain pre
11	545.5	78.5	131	D34904	Ig kappa chain pre
12	540.5	77.8	132	PH0106	Ig kappa chain pre
13	539	77.6	131	D29380	anti-digoxin trans
14	537.5	77.3	111	PS0074	Ig kappa chain pre
15	537.5	77.3	131	G34903	Ig kappa chain v r
16	536.5	77.2	131	S09259	Ig kappa chain pre
17	529.5	76.2	131	S52449	Ig kappa chain pre
18	523.5	75.3	131	PT0178	Ig kappa chain v r
19	521	75.0	130	C29380	Ig kappa chain pre
20	502	72.2	133	S23230	Ig kappa chain pre
21	497.5	71.6	119	A49032	Ig kappa chain v r
22	496	71.4	142	S22902	Ig kappa chain v r
23	493.5	71.0	118	S24503	Ig kappa chain v r
24	493	70.9	133	S42611	HUNK protein prec
25	492.5	70.9	118	S24536	Ig kappa chain v r
26	491	70.6	133	K2HURP	Ig kappa chain pre
27	490.5	70.6	118	S24533	Ig kappa chain v r
28	489	70.4	112	E27887	Ig kappa chain v r
29	488.5	70.3	118	S24500	Ig kappa chain v r

ALIGNMENTS

RESULT 1

B25912
Ig kappa chain precursor V region (W3129) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C:Accession: B25912
R:Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A:Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light
A:Reference number: A94147; MUID:87175689
A:Accession: B25912
A:Molecule type: mRNA
A:Residues: 1-132 <BOR>
A:Cross-references: GB:M15874; NID:g196639; PIDN:AAA38796.1; PID:g1966840
A:Note: the authors translated the codon CTC for residue 120 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence (fragment) #status predicted <SIG>
F:20-132/Product: Ig kappa chain V region W3129 #status predicted <VAR>
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 620; DB 2; Length 132;
Best Local Similarity 90.8%; Pred. No. 2.3e-47;
Matches 118; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 3 LPVRLVLLFWIPVSGDVVVTQTPLSLPVSTFGDQVSTICRSTSSQSLAKSYGNTYLSWYL 62
DB 2 LPVRLVLLFWIPVSGDVVVTQTPLSLPVSTFGDQVSTICRSTSSQSLAKSYGNTYLSWYL 61
QY 63 HKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTFTLKIKTPEDLGMVYCLQGTHTPVT 122
DB 62 HKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTFTLKIKTPEDLGMVYCLQGTHTPVT 121
QY 123 FGGGTGLEIK 132
DB 122 FGGGTGLEIK 131

RESULT 2

H30560
Ig kappa chain V region (36.1.2D) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: H30560
R:Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono
A:Reference number: A30560; MUID:89110062
A:Accession: H30560
A:Status: preliminary

Query Match 81.0%; Score 563; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.8e-42;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DVVVTQPLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80
|||||
DB 1 DVVVTQPLSLPVSGDQVSISSRSQSLANSYGNTLSWYLHKPGQSPQLLIYGISNRF 60
|||||

QY 81 SGVPDRFSGSGTDFTLKISIKPKEDLGMYYCLOQTHQPTFTGGGTKLEIK 132
|||||
DB 61 SGVPDRFSGSGTDFTLKISIKSEDLGMYYCLOQTHQPTFTGGGTKLEIK 112
|||||

RESULT 5
B39276
Ig light chain precursor V-D-J region (6-19) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: B39276
R:Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A:Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis
A:Reference number: A39276; MUID:91088540
A:Accession: B39276
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <REL>
A:Cross-references: GB:M55313; NID:g198095; PIDN:AAA63385.1; PID:g198096
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 560.5; DB 2; Length 131;
Best Local Similarity 80.3%; Pred. No. 3.5e-42;
Matches 106; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLVLPVSGDVVVTQPLSLPVSGDQVSISSRSQSLAKSYGNTYLSW 60
|||||
DB 1 MKLPVRLVLLVLPVSGDVVVTQPLSLPVSGDQVSISSRSQSLAKSYGNTYLSW 59
|||||

QY 61 YLHKPGQSPQLLIYGISNRFSGVPDRFSGSGTDFTLKISTIKPEDLGMYYCLOQTHQP 120
|||||
DB 60 YLQKPGQSPKLLIYKVNSRFSGVPDRFSGSGTDFTLKISRVEADLGVYYFCQGSHPV 119
|||||

QY 121 YTFGGGTKLEIK 132
|||||
DB 120 YTFGGGTKLEIK 131
|||||

RESULT 6
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; H34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-
A:Reference number: A34903; MUID:90094387
A:Accession: B34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PIDN:AAA61589.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 553.5; DB 2; Length 131;

C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 546.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 5.9e-41;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFWIPASSDDVMTQTPLSLPVSLGDAQISICRSQSLVHSGNTYLSW 59
QY 61 YLHKPGQ3PQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHP 120
DB 60 YLQKPGQ3PKLLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
QY 121 YTFGGGTLEIK 132
DB 120 FTFGGTLEIK 131

RESULT 11
D34904
Ig kappa chain precursor V region (3-13) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C:Accession: D34904
R:Bedzyk, W.D.; Harron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reactive V region of mouse immunoglobulin V region
A:Reference number: A34903; MUID:90094387
A:Accession: D34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:Cross-reference: GB:I39105; NID:9639658; PIDN:AAAG1590.1; PID:9639659
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 545.5; DB 2; Length 131;
Best Local Similarity 78.8%; Pred. No. 7.2e-41;
Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFWIPASSDDVMTQTPLSLPVSLGDAQISICRSQSLVHSGNTYLSW 59
QY 61 YLHKPGQ3PQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHP 120
DB 60 YLQKPGQ3PKLLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
QY 121 YTFGGGTLEIK 132
DB 120 FTFGGTLEIK 131

RESULT 12
PH0106
anti-digoxin transfectoma antibody heavy chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C:Accession: PH0106
R:Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
Mol. Immunol. 27, 901-909, 1990
A:Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain
A:Reference number: PH0105; MUID:91015092
A:Accession: PH0106
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <NEA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 540.5; DB 2; Length 132;
Best Local Similarity 79.5%; Pred. No. 2e-40;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFWIPASSDDVMTQTPLSLPVSLGDAQISICRSQSLVHSGNTYLSW 59
QY 61 YLHKPGQ3PQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHP 120
DB 60 YLQKAGQ3PKLLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
QY 121 YTFGGGTLEIK 132
DB 120 FTFGGTLEIK 131

RESULT 13
D29380
Ig kappa chain precursor V region (B003 46/2D7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C:Accession: D29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable region of mouse immunoglobulin V region
A:Reference number: A92612; MUID:88007582
A:Accession: D29380
A:Molecule type: mRNA
A:Residues: 1-131 <CHE>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-113/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 539; DB 2; Length 131;
Best Local Similarity 78.8%; Pred. No. 2.6e-40;
Matches 104; Conservative 8; Mismatches 18; Indels 2; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFWIPASSDDVMTQTPLSLPVSLGDAQISICRSQSLVHSGNTYLSW 58
QY 61 YLHKPGQ3PQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHP 120
DB 59 YLQKPGQ3PKLLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHLP 118
QY 121 YTFGGGTLEIK 132
DB 119 RTFGGTLEIK 130

RESULT 14
PS0074
Ig kappa chain V region (38C13.V7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0074
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement of the immunoglobulin V region
A:Reference number: A92781; MUID:89310348
A:Accession: PS0074
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-111 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 537.5; DB 2; Length 111;
Best Local Similarity 92.9%; Pred. NO. 3e-40;
Matches 104; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 21 DVVVTTQTPLSLPVDFGDQVSIICRSSQLAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 80

1 DVVVVTOTPLSLPVSEFGDOVSTICRSSLANSSYGNTRYLSWY LHKPGOSPOLLTYGTSNRF 60

Qy 81 SGVPDRFSGSGGTDFTLKISTIKPEDLGMYCYLQGTHQPYTFGGGTKLEIK 132

db 61 SGVPBREGSGSGSTOETIKISTIKBEDIGWVYCILOSTHO-ITEGACTKIEIK 111

RESULT 15

G34903

Ig kappa chain precursor V region (10-25) - mouse

C; Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000

C;Accession: G34903

R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A;Title: Active site structure and antigen binding properties of idiotypically cross-reacting

A; Reference number: A34903; MUID: 90094387

A; Accession: G34903

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-131 <BED>

A;Cross-references: GB:M32381; GB:J05237; GB:J05238; NID:g639654; PIDN:AAA61588.1; PID:g

C: Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 537.5; DB 2; Length 131;
Best Local Similarity 78.0%; Pred. No. 3.6e-40;
Matches 103; Conservative 9; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MKLPVRLVLLFWIPVSGGDVVVTQTPLSLPVSGDQVSI~~CRSSQSLAKSYGNT~~YLSW 60

db 1 MKLPVRLV-I-MFWIPASSSSNVMTOTPI SLPVSLCDOASISCPSSOSLTHSNCNTVEHW 59

QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDETLKISTIKPEDLGMYCLOGTHOP 120

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Search completed: April 13, 2001, 15:36:46
Job time: 133 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:40:18 ; Search time 21.32 Seconds
(without alignments)
212.088 Million cell updates/sec

Title: US-08-700-737-12
Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOCTHQPYFGGCKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	70.6	133	1	KV2F_HUMAN
2	471	67.8	113	1	KV2G_MOUSE
3	422	60.7	117	1	KV2E_HUMAN
4	418	60.1	113	1	KV2D_HUMAN
5	416.5	59.9	115	1	KV2A_HUMAN
6	410	59.0	113	1	KV2B_HUMAN
7	401	57.7	129	1	KV3L_HUMAN
8	400	57.6	129	1	KV3M_HUMAN
9	395.5	56.9	112	1	KV2C_HUMAN
10	395	56.8	112	1	KV2F_MOUSE
11	394	56.7	113	1	KV2D_MOUSE
12	392	56.4	113	1	KV2E_MOUSE
13	387.5	55.8	131	1	KV3I_MOUSE
14	385.5	55.5	134	1	KV4C_HUMAN
15	380.5	54.7	128	1	KV3K_HUMAN
16	378	54.4	133	1	KV4B_HUMAN
17	373.5	53.7	132	1	KV3F_MOUSE
18	372	53.5	120	1	KV2B_MOUSE
19	369	53.1	113	1	KV2C_MOUSE
20	368	52.9	129	1	KV3H_HUMAN
21	367	52.8	112	1	KV2A_MOUSE
22	366.5	52.7	136	1	KV5B_MOUSE
23	359.5	51.7	111	1	KV3H_MOUSE
24	356.5	51.3	111	1	KV3L_MOUSE
25	356.5	51.3	129	1	KV1W_HUMAN
26	354.5	51.0	114	1	KV4A_HUMAN
27	353.5	50.9	115	1	KV3I_HUMAN
28	352.5	50.7	108	1	KV1_CANFA
29	350.5	50.4	111	1	KV3Q_MOUSE
30	350.5	50.4	149	1	KV5A_MOUSE
31	347.5	50.0	128	1	KV5E_MOUSE
32	346.5	49.9	111	1	KV3M_MOUSE
33	345.5	49.7	129	1	KV1X_HUMAN

34	345	49.6	108	1	KV3A_HUMAN	P01619	homo sapien
35	345	49.6	109	1	KV3B_HUMAN	P01620	homo sapien
36	344.5	49.6	111	1	KV3A_MOUSE	P01654	mus musculus
37	344	49.5	116	1	KV3J_HUMAN	P04434	homo sapien
38	343.5	49.4	111	1	KV3Q_MOUSE	P01667	mus musculus
39	341.5	49.1	108	1	KV1M_HUMAN	P01605	homo sapien
40	341.5	49.1	111	1	KV3D_MOUSE	P03977	mus musculus
41	340.5	49.0	111	1	KV3N_MOUSE	P01666	mus musculus
42	340	48.9	112	1	KV3B_MOUSE	P01655	mus musculus
43	339.5	48.8	111	1	KV3C_MOUSE	P01656	mus musculus
44	338.5	48.7	111	1	KV3Q_MOUSE	P01669	mus musculus
45	338.5	48.7	111	1	KV3R_MOUSE	P01670	mus musculus

ALIGNMENTS

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RESULT 1
KV2F_HUMAN
ID   KV2F_HUMAN          STANDARD;          PRT;          133 AA.
AC   P06310;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8601852; PubMed=2997711;
RA   Klobbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III."
RL   Nucleic Acids Res. 13:6499-6513(1985).
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; Z00020; CAA77315.1; -
DR   PIR; A01890; K2HURP.
DR   InterPro; IPR003006; -
DR   Pfam; PF000047; Ig_1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL              1..20
FT   CHAIN               21..133
FT   DOMAIN              21..43
FT   DOMAIN              44..59
FT   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN              60..74
FT   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN              75..81
FT   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN              82..113
FT   COMPLEMENTARITY-DETERMINING 4.
FT   DOMAIN              114..122
FT   DISULFID            43..113
FT   NON_TER             133..133
SQ   SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

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IG KAPPA CHAIN V-II REGION RPMI 6410.

FRAMEWORK 1.

COMPLEMENTARITY-DETERMINING 1.

FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING 2.

FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING 3.

FRAMEWORK 4.

BY SIMILARITY.

SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match

Best Local Similarity 70.6%; Score 491; DB 1; Length 133;

Matches 91; Conservative 19; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLPVPSFGDVQVSIICRSSQSLAKSYGNTYLSW 60

Db 1 MRUPAQLGLLMLVPGSGDVVVTQTPLPVPSFGDVQVSIICRSSQSLAKSYGNTYLSW 60

QY 61 YLHKPQSPQLIYIGISNRFSGVDPDRFSGSGCTDFTLKISTIKPEDLGMVYCLQGTQHP 120

RX MEDLINE=84191506; PubMed=6325927;
 RA Klobbeck H.G., Solomon A., Zachau H.G.;
 RT "Contribution of human V kappa II germ-line genes to light-chain
 RL diversity";
 CC Nature 309:73-76(1984).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z00009; NOT_ANNOTATED_CDS.
 DR PIR: A01889; K2HUGM;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 1;
 DR Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
 FT DOMAIN 27 FRAMEWORK 1.
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 44 58 FRAMEWORK 2.
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 66 97 FRAMEWORK 3.
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 107 116 FRAMEWORK 4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

 Query Match 60.7%; Score 422; DB 1; Length 117;
 Best Local Similarity 71.3%; Pred. No. 2.2e-35;
 Matches 82; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

 QY 18 SGSDVVTQPLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHKGQSPOLLYIGIS 77
 DB 2 SSGDIVMTQSPISLPTVTPGEPASISCRSSQSLHSGNYNLDWYLOKPOQSOLLILYGS 61

 QY 78 NRESGVDPDRFSGSGCTDFTLKISTIKPEDLGMYYCLOGTHQPTFGGKLEIK 132
 DB 62 NRASGVDPDRFSGSGCTDFTLKISRVEAEDGVIYVCMQGLQTPQTGQGTKEIK 116

 RESULT 4
 ID KV2D_HUMAN STANDARD; PRT: 113 AA.
 AC P01617;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION TEW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RA MEDLINE=74148480; PubMed=4596149;
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
 RA "Amino acid sequence of a kappa Bence Jones protein from a case of
 RT primary amyloidosis";
 RL Biochemistry 12:3763-3780(1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RA MEDLINE=73166638; PubMed=4700495;
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
 RA Glenner G.G.;
 RA "Structural identity of Bence Jones and amyloid fibril proteins in a
 RT patient with plasma cell dyscrasia and amyloidosis.";

Db 61 FQORPCQ:PRRLIYKVSNRDGVDPDRFSGSGTDTLTKISRVEAEDGVYVCMQGTIHS 120
 QY 121 YTFGGTILEIK 132
 Db 121 WTFGGTILEIK 132

 RESULT 2
 KV2G_MOUSE STANDARD; PRT: 113 AA.
 ID P01631;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION 26-10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=83173921; PubMed=6404298;
 RA Novotny J., Margolies M.N.;
 RT "Amino acid sequence of the light chain variable region from a mouse
 RT anti-digoxin hybridoma antibody.";
 RL Biochemistry 22:1153-1158(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
 CC PROTEIN THAT BINDS DIGOXIN.
 DR PIR: A01914; KVMS26;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 1;
 DR Immunoglobulin V region; Monoclonal antibody; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

 Query Match 67.8%; Score 471; DB 1; Length 113;
 Best Local Similarity 80.4%; Pred. No. 2.9e-40;
 Matches 90; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

 QY 21 DWVVTQ:PLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHKGQSPOLLYIGISNRF 80
 DB 1 DVVVTQ:PLSLPVSLGDAQSISCRSSQSLHSGNYNLDWYLOKAGQSPKLLIYKVSNRF 60

 QY 81 SGVDPDR:SGSGSGTDTLTKISTIKPEDLGMYYCLOGTHQPTFGGKLEIK 132
 DB 61 SGVDPDR:SGSGSGTDTLTKISRVEAEDGLIYFCSTTHVPTFGGKLEIK 112

 RESULT 3
 KV2E_HUMAN STANDARD; PRT: 117 AA.
 ID P06309;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1.2)
CC MARKER.
DR PIR; A01886; K2HUTW.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 60.1%; Score 418; DB 1; Length 113;
Best Local Similarity 69.6%; Pred. No. 5.4e-35;
Matches 78; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
QY 21 DVVVTQPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPKQSPOLLIIYISNRF 80
DB 1 DIVMTQSPFLPVTGEPASISCRSSQSLHSDGFDYLNWYLRKQKQSPZLLIYALSNA 60
QY 81 SGVPDRFSGSGGTDFTLKISTIKPEDLGMYCYCLOGTHQPTFGGKLEIK 132
DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMZALQAPITFGGKLEIK 112

RESULT 5
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION CUM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=68242259; PubMed=5586923;
RX Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4181819;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 59.9%; Score 416.5; DB 1; Length 115;
Best Local Similarity 69.6%; Pred. No. 5.4e-35;
Matches 78; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Best Local Similarity 72.6%; Pred. No. 7.8e-35;
Matches 82; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
QY 21 DVVVTQPLSLPVSGDQVSISSCRSSQSLAKS-YNTYLSWYHLKPKQSPOLLIIYISNRF 79
DB 2 DIVMTQSPFLPVTGEPASISCRSSQSLHSDGFDYLNWYLRKQKQSPZLLIYALSNA 61
QY 80 FSGVPDRFSGSGGTDFTLKISTIKPEDLGMYCYCLOGTHQPTFGGKLEIK 132
DB 62 ASGVPDRFSGSGGTDFTLKISRVEADGVVYCMZALQAPITFGGKLEIK 114

RESULT 6
KV2B_HUMAN
ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenström's
IgM
Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUF.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 59.0%; Score 410; DB 1; Length 113;
Best Local Similarity 68.8%; Pred. No. 3.4e-34;
Matches 77; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
QY 21 DVVVTQPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPKQSPOLLIIYISNRF 80
DB 1 DVVMTQSPFLPVTGEPASISCRSSQSLVYRGTLYLNWYLRKQKQSPZLLIYALSNA 60
QY 81 SGVPDRFSGSGGTDFTLKISTIKPEDLGMYCYCLOGTHQPTFGGKLEIK 132
DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMZALQAPITFGGKLEIK 112

RESULT 7
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

Sat Apr 14 08:10:20 2001

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NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=89171307; PubMed=3127527;
Klips T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
LEUKEMIA.
CC PIR: PLO022; K3HUHA.
DR HSP: P01789; 2MCP.
DR InterPro: IPI003006; -.
DR Pfam: PF00047; ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 57.7%; Score 401; DB 1; Length 129;
Best Local Similarity 56.8%; Pred. No. 3.1e-33;
Matches 75; Conservative 27; Mismatches 26; Indels 4; Gaps 1;

QY 1 MKLPVRLVLLLEWIPVSGDVVVTQPLSLPVSFGDQVSIKRSQSLAKSYGNTYLSW 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 METPAQLLFLLLWLPDPTTGTEIVLTQSPGTLSPGERATLSCRAQSVSS---YLAW 56

QY 61 YLHRPGSPQLLYIGINRFSVDPDRFSGSGGTDFTLTKISTIKPEDLGMVYCLQGTTHP 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 YQKPGCAPRLIYIGASSRATGIPDRFSGSGGTDFTLTKISTIKPEDLGMVYCLQGTSP 116

QY 121 YTEGGGKLEIK 132
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 YTFGGGKVEIK 128

RESULT 8
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89171307; PubMed=3127527;
RA Klips T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
LEUKEMIA.
CC PIR: PLO021; K3HUHI.
DR HSP: P01789; 2MCP.

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QY 21 DVVVTQPLSLPVSGDQVTSICRSSLAKSYGNTYLSWYLNKPGQSPQLLIYGISNRF 80
DB 1 DIVLTQSPFLSLPVTPGEPASISCRSSQNLZSGBG-YLDWYLZKPGSPZLLIYLSGNRA 59

QY 81 SGVPDRFSGSGGDTFTLKISTIKPEDLGMYYICLQGHQPTFTGGGKLEIK 132
DB 60 SGVPNRFSGSGGTBFTLKISRVA2BVGYYCMAQLQTPLTFTGGGTNVEIK 111

RESULT 10
KV2D_MOUSE STANDARD; PRT; 112 AA.
AC P01629;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 2S1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=83055101; PubMed=7141411;
RX Herbst H., Chang J.Y., Abersold R., Braun D.G.;
RA "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
RT the group A streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01911; KVMSS1.
DR InterPro: IPR003006;
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 FRAMEWORK 2.
FT DOMAIN 40 54 FRAMEWORK 3.
FT DOMAIN 55 61 FRAMEWORK 4.
FT DOMAIN 62 93 BY SIMILARITY.
FT DOMAIN 94 102 FRAMEWORK 1.
FT DISULFID 103 112 FRAMEWORK 2.
FT NON_TER 112 112 FRAMEWORK 3.
FT SEQUENCE 112 AA; 12221 MW; BD5EF56D789FBEC CRC64;

Query Match 56.8%; Score 395; DB 1; Length 112;
Best Local Similarity 67.9%; Pred. No. 1e-32;
Matches 76; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 21 DVVVTQPLSLPVSGDQVTSICRSSLAKSYGNTYLSWYLNKPGQSPQLLIYGISNRF 80
DB 1 DIVVTQAFNPVTLGTSFSCRSKSLQSGKITLYWYLNKPGQSPQLLIYQMSNLA 60

QY 81 SGVPDRFSGSGGDTFTLKISTIKPEDLGMYYICLQGHQPTFTGGGKLEIK 132
DB 61 SGVPDRFSGSGGDTFTLRSRVEADVGYIYCANLQELPYTFTGGGKLEIK 112

RESULT 11
KV2F_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP MEDLINE=83256427; PubMed=6409088;
RX Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RA "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoozobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR InterPro: IPR003006;
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 FRAMEWORK 2.
FT DOMAIN 40 54 FRAMEWORK 3.
FT DOMAIN 55 61 FRAMEWORK 4.
FT DOMAIN 62 93 BY SIMILARITY.
FT DOMAIN 94 102 FRAMEWORK 1.
FT DISULFID 103 112 FRAMEWORK 2.
FT NON_TER 112 112 FRAMEWORK 3.
FT SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 56.7%; Score 394; DB 1; Length 113;
Best Local Similarity 67.9%; Pred. No. 1.3e-32;
Matches 76; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 21 DVVVTQPLSLPVSGDQVTSICRSSLAKSYGNTYLSWYLNKPGQSPQLLIYGISNRF 80
DB 1 DIVVTQAPSAVTPGESVSICRSKSLHNSGNTLYWFLQRPQCQLLIYRMSNLA 60

QY 81 SGVPDRFSGSGGDTFTLKISTIKPEDLGMYYICLQGHQPTFTGGGKLEIK 132
DB 61 SGVPDRFSGSGGDTFTLRSRVEADVGYIYCANLQELPYTFTGGGKLEIK 112

RESULT 12
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=85128968; PubMed=6441768;
RX Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RA "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.
DR InterPro: IPR003006;
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 FRAMEWORK 2.
FT DOMAIN 40 54 FRAMEWORK 3.
FT DOMAIN 55 61 FRAMEWORK 4.
FT DOMAIN 62 93 BY SIMILARITY.
FT DOMAIN 94 102 FRAMEWORK 1.
FT DISULFID 103 112 FRAMEWORK 2.
FT NON_TER 112 112 FRAMEWORK 3.
FT SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

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FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 56.4%; Score 392; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 2.le-32;
Matches 75; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

QY 21 DVVVTQTLISLPVSGDQVSIQSSQSLAKSYGNTYLSWYHLKPGQSPOLLIIYGISNRF 80
   |::|| |::| |::||::|| |::|| |::|| |::|| |::|| |::|| |::||
DB 1 DLIVTQAFNSPVTLGTSASISCRSKSLHSHNGITYLWYLYKQFGQSPOLLIIYQNSILA 60
   ||::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
QY 81 SGVPDRFSGSGDTFTLKISTIKPEDLGMYCLOGTHQPTFFGGGKLEIK 132
   ||::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
DB 61 SGVPDRFSGSGDTFTLRISRVEADGVYCAHNLELPYFFGGGKLEIK 112
   ||::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||

RESULT 13
KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=1090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78231887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 31-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79015520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR InterPro: IPI003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 55.8%; Score 387.5; DB 1; Length 131;
Best Local Similarity 56.8%; Pred. No. 7e-32;
Matches 75; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

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Matches 75; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDQVSVITQTPLSLPVSGDQVSIQSSQSLAKSYGNTYLSW 60
   |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
DB 1 METDTLLLVLLWVPGSTGNIVLTQSPASLAVSLGQRATISCRASESV-DSYGNSEMH 59
   |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
QY 61 YLHKFGQSPOLLIIYGISNRFSGVGPDRFSGSGDTFTLKISTIKPEDLGMYCLOGTHQ 120
   |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
DB 60 YQKFGQSPKLLIYLASNLESGVPAFSGSGRTFTLTIDPVEADDAATYYCQNNEDP 119
   |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
QY 121 YTFGGGKLEIK 132
   |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||
DB 120 WTFGGGKLEIK 131
   |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||

RESULT 14
KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X02990; CAA26733.1; -.
DR PIR; A01905; K4HU17.
DR HSP; P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 133 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 55.5%; Score 385.5; DB 1; Length 134;
Best Local Similarity 57.1%; Pred. No. 1.le-31;
Matches 76; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDQVSVITQTPLSLPVSGDQVSIQSSQSLAKSYGNTYLS 59
   |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::||

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Db 1 MVLQTVFISLLWISGVDIVMTQSPDSLAVSLGERATINCKSSQSIYSSDNKNYLA 60
QY 60 WYLHKPGSQPLLIIYGINRFSGVDPDRSGSGGTDFTLKISTIRPEDLGMYYCLOGTHQ 119
Db 61 WYQKPGQPPLLIIYWAISTRESGVDPDRSGSGGTDFTLTISLQAEADVAVYCOQYVNL 120
QY 120 PYTFGGGKLEIK 132
Db 121 PWTFGGKVEIK 133

RESULT 15
KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC -----
DR EMBL; 200021; CAA7316.1; -
DR PIR; A01899; K3HU41.
DR InterPro; IPR003006; -
DR Pfam; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 54.7%; Score 380.5; DB 1; Length 128;
Best Local Similarity 55.3%; Pred. No. 3.4e-31;
Matches 73; Conservative 26; Mismatches 28; Indels 5; Gaps 1;

Qy 1 MKLPVRLVLLWLPVSGDVVYVQTPLSLFVSGDVISCRSSQSLAKSYGNTYLSW 60
Db 1 METPAQLLFLLLWLPDPTTGIVLTQSPGTLSLSPGESATLSCRASQSVSN-----LAW 55
QY 61 YLHKPGSQPLLIIYGINRFSGVDPDRSGSGGTDFTLKISTIRPEDLGMYYCLOGTHQ 120
Db 56 YQKRGOSPRLLIRINDASSRANGIPDRFSGGSGTDFTLTISRLEPEDFAVYCOQYSTSP 115
QY 121 YTFGGGKLEIK 132
Db 116 YTFGGGKLEIK 127
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Search completed: April 13, 2001, 15:40:18
Job time: 271 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:39:52 ; Search time 56.51 Seconds
(without alignments)
273.782 Million cell updates/sec

Title: US-08-700-737-12
Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHOPYFGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	447	64.3	104	11 Q9JL82	Q9JL82 mus musculus
2	412.5	59.4	114	4 Q9UL80	Q9UL80 homo sapien
3	356	51.2	109	4 Q9UL78	Q9UL78 homo sapien
4	334.5	48.1	108	4 Q9UL77	Q9UL77 homo sapien
5	326.5	47.0	298	11 Q9QYF0	Q9QYF0 mus musculus
6	326	46.9	109	4 Q9UL86	Q9UL86 mus musculus
7	323.5	46.5	108	4 Q9UL70	Q9UL70 mus musculus
8	319.5	46.0	99	11 Q9JL74	Q9JL74 mus musculus
9	319.5	46.0	108	4 Q9UL79	Q9UL79 mus musculus
10	319.5	46.0	214	11 Q9R1A5	Q9R1A5 mus musculus
11	315	45.3	109	4 Q9UL85	Q9UL85 mus musculus
12	314.5	45.3	103	11 Q9JL80	Q9JL80 mus musculus
13	311.5	44.8	108	4 Q9UL83	Q9UL83 mus musculus
14	310	44.6	107	4 Q9UL81	Q9UL81 mus musculus
15	295	42.4	106	5 Q9U410	Q9U410 schistosoma
16	287.5	41.4	101	11 Q9JL78	Q9JL78 mus musculus
17	279.5	40.2	107	11 Q9JL84	Q9JL84 mus musculus
18	263.5	37.9	97	11 Q9JL76	Q9JL76 mus musculus
19	249.5	35.9	109	6 Q9NOW5	Q9NOW5 oryctolagus

20	227	32.7	107	4 Q9NSD6	Q9NSD6 homo sapien
21	209.5	30.1	130	4 Q9NP29	Q9NP29 homo sapien
22	206.5	29.7	107	4 Q9UL82	Q9UL82 homo sapien
23	148	21.3	509	11 Q9QX57	Q9QX57 mus musculus
24	148	21.3	513	11 P97797	P97797 mus musculus
25	146	21.0	509	11 Q9W907	Q9W907 mus musculus
26	137	19.7	509	11 Q9WTN4	Q9WTN4 mus musculus
27	132.5	19.1	168	4 Q9UQ56	Q9UQ56 mus musculus
28	132.5	19.1	246	4 Q9UQ55	Q9UQ55 mus musculus
29	126.5	18.2	123	11 Q61243	Q61243 mus musculus
30	125.5	18.1	210	6 P79336	P79336 felis silve
31	119.5	17.2	509	11 P97710	P97710 rattus norv
32	118.5	17.1	93	4 Q9UL76	Q9UL76 mus sapien
33	117	16.8	123	4 Q9UKI3	Q9UKI3 mus sapien
34	115.5	16.6	418	11 Q70426	Q70426 rattus norv
35	115.5	16.6	509	11 Q9QW15	Q9QW15 rattus norv
36	114	16.4	116	4 Q9UL89	Q9UL89 mus sapien
37	111	16.0	209	6 Q9XSM7	Q9XSM7 salmirl sci
38	110.5	15.9	285	11 Q9JME9	Q9JME9 mus musculus
39	110	15.8	200	4 Q95776	Q95776 mus sapien
40	108	15.5	235	6 Q9XSM6	Q9XSM6 salmirl sci
41	107	15.4	397	4 Q9Y4V0	Q9Y4V0 mus sapien
42	105	15.1	337	13 Q9IB02	Q9IB02 sphoeroides
43	104.5	15.0	401	6 Q98835	Q98835 cercopithec
44	104	15.0	334	13 Q9IB05	Q9IB05 sphoeroides
45	104	15.0	506	6 Q46632	Q46632 bos taurus

ALIGNMENTS

RESULT 1

Q9JL82 ID Q9JL82 PRELIMINARY: PRT; 104 AA.
AC Q9JL82
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206024; AAF69322.1;
FT NON_TER 1
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match 64.3%; Score 447; DB 11; Length 104;
Best Local Similarity 80.8%; Pred. No. 4.3e-38;
Matches 84; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 29 LSLPVSGQDVSTSCSSQSLAKSYNTYLSWLHKPGQSPOLLTYGINSRFGVDPDRFS 88
Db 1 LSLPVSLGQASISCRSSQSLVHTNGTYLHWLQPGQSPKLLYKVSNRFGVDPDRFS 60
QY 89 GSGSGDFTLKISTIKPEDLGMVYCLQTHQPTFGGKLEIK 132
Db 61 GSGSGDFTLKISTIRVEAEDLVYFCSTQTHVPTFGGKLEIK 104

RESULT 2

Q9UL80 ID Q9UL80 PRELIMINARY: PRT; 114 AA.
AC Q9UL80;

[illegible]

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HALB/C; TISSUE=SPLEEN;
RD Shinochana N., Demura T., Fukuda H.;
RE "Isolation of a novel type of vascular cell wall-specific monoclonal
RF antibody recognizing a cell polarity using a phase display subtraction
RT method.";
RT

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB036341; BAA88633.1; -
 DR HSP: P01607; 1REI
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 2.
 SQ SEQUENCE 298 AA; 31867 MW; E0F9688A17004317 CRC64;

Query Match 47.0%; Score 326.5; DB 11; Length 298;
 Best Local Similarity 53.5%; Pred. No. 2.5e-25;
 Matches 61; Conservative 19; Mismatches 29; Indels 5; Gaps 1;
 Qy 19 GGDVVVOTPLSLPVSGDOVSICRSSLAKSYGNTYLSWYHLKPGQSPQLLIYGISN 78
 Db 171 GSDIELTQSPASLSVGETVITCRASGNI-----HNLAWYQKQKSPQLLIYNAKT 225
 Qy 79 RESGVPDRFSGSGTDTFLTKISTIKPEDLGMVYCLQGTHTQPTFGGGTKLEIK 132
 Db 226 LADGVPSRFSGSGGTQVSLKINSLSQPEDFGSYQCQHFWTPTPTFGGGTKLEIK 279

RESULT 6
 Q9UL86 PRELIMINARY; PRT; 109 AA.
 ID Q9UL86
 AC Q9UL86;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035028; AAD56284.1; -
 DR HSP: P01789; IMCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 46.9%; Score 326; DB 4; Length 109;
 Best Local Similarity 54.5%; Pred. No. 8.3e-26;
 Matches 61; Conservative 25; Mismatches 22; Indels 4; Gaps 1;
 Qy 21 DVVVTOTPLSLPVSGDOVSICRSSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 80
 Db 1 EIVLTQSPGTLSPFGERATLSRASQSVSSS---YLAWYQKQPGQAPRELIYGTSSRA 56
 Qy 81 SGVPDRFSGSGTDTFLTKISTIKPEDLGMVYCLQGTHTQPTFGGGTKLEIK 132
 Db 57 TGIPDRFSGSGSETDTLTISRLPEDFAVYQCQYGSISFTFGPGTKVDIK 108

RESULT 7
 Q9UL70 PRELIMINARY; PRT; 108 AA.
 ID Q9UL70
 AC Q9UL70;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035044; AAD56280.1; -
 DR HSP: P01607; 1REI
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 1.
 FT NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 46.5%; Score 323.5; DB 4; Length 108;
 Best Local Similarity 56.2%; Pred. No. 1.5e-25;
 Matches 63; Conservative 17; Mismatches 27; Indels 5; Gaps 1;
 Qy 21 DVVVTOTPLSLPVSGDOVSICRSSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 80
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQGI-----SNLYAWYQKQKPKSLIYAASLTQ 55
 Qy 81 SGVPDRFSGSGTDTFLTKISTIKPEDLGMVYCLQGTHTQPTFGGGTKLEIK 132
 Db 56 SGVPSRFSGSGTDTLTISLQPEDVATYVCQKYNAPRTFGPGTKLEIK 107

RESULT 8
 Q9JL74 PRELIMINARY; PRT; 99 AA.
 ID Q9JL74
 AC Q9JL74;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206032; AAF69330.1; -
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match 46.0%; Score 319.5; DB 11; Length 99;
 Best Local Similarity 59.8%; Pred. No. 3.4e-25;
 Matches 61; Conservative 17; Mismatches 19; Indels 5; Gaps 1;
 Qy 31 LPVSFGDOVSICRSSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRFSGVPDRFSGS 90
 Db 3 LLVSAGDRVTITCRASQSVSND-----VAWYQKQKPGSPKLLIYASNRVYGVDPDRFTGS 57
 Qy 91 GSGTDTFLTKISTIKPEDLGMVYCLQGTHTQPTFGGGTKLEIK 132
 Db 58 GYGTDTFTTSTQAEADLAVYFCQDYSSPRTFGGGTKLEIK 99
 RESULT 9
 Q9UL79 PRELIMINARY; PRT; 108 AA.
 ID Q9UL79

Db 1 DIQLTDFSGSGSMTASGERVITITCKASQDI-----NSVLSWFQQPGKSPKTLIYRANRLV 55
 QY 81 SGVDFRFGSGSGTDTLTKISTIKPEDLGMVYCLQGHOPVTFGGGPKLEIK 132
 Db 56 DGVPSRFGSGSGQDYSUTISSLEYEDMGIIYCLQYDEFFTFGSGTKLEIK 107

RESULT 11
 Q9JL80 PRELIMINARY; PRT; 109 AA.
 ID Q9JL85
 AC Q9JL85;
 DT 01-MAY-2000 (TREMBLrel..13, Created)
 DT 01-MAY-2000 (TREMBLrel..13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel..15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035029; AAD56265.1; -
 DR HSP: P01607; 1REI.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; ig; 1.
 DR NON_TER 1
 FT NON_TER 109
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11761 MW; FBIE43E7C7AFACCC CRC64;

Query Match 45.3%; Score 315; DB 4; Length 109;
 Best Local Similarity 53.1%; Pred. No. 1.le-24;
 Matches 60; Conservative 26; Mismatches 21; Indels 6; Gaps

QY 21 DVVVTQPLSPVSGDOVSISCRSSQSLAKSVGNVYLSWYLHKPGQSPQLLIYGISNRF 80
 Db 1 EIVMTQSPATLSVSPGERATLSCWASQSSIN-----LAWYQKPGQAPRLLIYGASTRA 55

QY 81 SGVDFRFGSGSGTDTLTKISTIKPEDLGMVYCLQ-GTHOPTVTFGGGPKLEIK 132
 Db 56 TGIPAREFGSGSGTEFTLTSSLSQSDFAIYHCQQYNWPLPTFGGKTVEIK 108

RESULT 12
 Q9JL80 PRELIMINARY; PRT; 103 AA.
 ID Q9JL80
 AC Q9JL80;
 DT 01-OCT-2000 (TREMBLrel..15, Created)
 DT 01-OCT-2000 (TREMBLrel..15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel..15, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALB/C;
 RA Markiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206026; AAF69324.1; -
 FT NON_TER 1
 FT NON_TER 103
 SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: April 13, 2001, 15:35:37 ; Search time 57.59 Seconds
(without alignments)
131.022 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPYFGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.*
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7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	695	100.0	132	19 W53814	Murine Act-1 light
2	695	100.0	140	19 W53817	Consensus protein
3	608	87.5	138	19 W53812	Light chain of a h
4	559.5	80.5	238	18 W14942	3F4 Human IgG4 exp
5	559.5	80.5	238	18 W14937	Murine anti-porcine
6	558.5	80.4	131	18 W34518	Variable kappa cha
7	554.5	79.8	149	17 W03199	Anti-idiotypic mono
8	554.5	79.8	149	20 Y21545	Monoclonal antibod
9	552.5	79.5	149	20 Y49209	MAB 1A7 light chai
10	552.5	79.5	149	20 Y28468	Light chain variab
11	550.5	79.2	131	21 B23812	Plasmid pGEM-MIL m

12	548.5	78.9	131	15	R52772	Murine KC-4 immuno
13	548.5	78.9	131	15	R52790	Murine KC-4 immuno
14	548.5	78.9	131	16	R70457	VL sequence of ant
15	546.5	78.6	238	20	Y17416	Mouse immunoglobul
16	543.5	78.2	131	14	R32241	Chimeric MAB light
17	543.5	78.2	131	14	R31587	BR55-2 light chain
18	537.5	77.3	131	14	R32245	BR55-2 murine IgG3
19	537.5	77.3	131	15	R52822	Humanised murine K
20	537.5	77.3	131	16	R70470	Humanised anti-KC-
21	535.5	77.1	132	19	W60867	Variable region of
22	535.5	77.1	132	21	Y80294	IgM chimeric antib
23	535.5	77.1	238	18	W31752	L chain subunit of
24	535.5	77.1	238	19	W71889	Anti-human Fas mon
25	535.5	77.1	238	21	B12909	Anti-human Fas ant
26	530.5	76.3	131	21	B23814	Plasmid pGEM-W2L m
27	529.5	76.2	140	19	W68492	Variable light cha
28	527.5	75.9	172	12	R15199	R6-5-D6 anti-ICAM-
29	523	75.3	150	12	R11598	Murine monoclonal
30	519.5	74.7	131	15	R52788	Murine BrE-3 immu
31	519.5	74.7	131	15	R52770	Murine BrE-3 immu
32	517.5	74.5	131	11	R09424	Co-1 Light Chain V
33	517.5	74.5	131	18	W06214	MAB Co-1 light cha
34	513	73.8	127	19	W76124	Murine ICR-8.1 V-K
35	513	73.8	127	19	W71254	Murine antibody IC
36	513	73.8	127	20	Y00781	Murine antibody IC
37	513	73.8	127	20	W81448	Antibody against I
38	513	73.8	127	21	B13044	Murine antibody IC
39	513	73.8	127	21	Y82443	Murine ICR-8.1 ant
40	513	73.8	127	21	Y50751	Murine antibody IC
41	511.5	73.6	131	15	R52806	Humanised murine B
42	511.5	73.6	131	20	W85060	Mouse Co-1 light c
43	509	73.2	132	19	W50219	Amino acid sequenc
44	506.5	72.9	173	12	R15059	Murine anti-ICAM m
45	503	72.4	239	19	W71876	Anti-human Fas hum

ALIGNMENTS

RESULT 1
W53814
ID W53814 standard; Protein; 132 AA.
XX
AC W53814;
XX
DT 14-JUL-1998 (first entry)
XX
DE Murine Act-1 light chain variable region.
XX
KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW Inflammatory bowel disease.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /note= "signal peptide"
FT /note= "mature protein"
XX
W09806248-A2.
PN
XX
XX
PD 19-FEB-1998.
XX
PF 06-AUG-1997; 97WO-US13884.
XX
PR 15-AUG-1996; 96US-0700737.
XX
PA (LEUK-) LEUKOSITE INC.
XX

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PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
PI Saldanha J;
XX WPI: 1998-15172/14.
XX N-PSDB: V2007.
XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
XX used for treating inflammatory disease, pancreatitis, diabetes,
XX asthma, graft versus host disease and sarcoidosis
XX
XX Claim 23; Fig 7; 145pp; English.
XX
XX The present sequence represents the light chain variable region of
XX murine antibody Act-1. Act-1 is active against human alpha4-beta7
XX integrin. Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a
XX ligand of this particular integrin. The Act-1 antibody interferes with
XX alpha4-beta7 integrin binding to MacCAM-1, which is present of high
XX endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used
XX to inhibit the interaction of cells bearing alpha4-beta7 with cells
XX bearing a ligand for alpha4-beta7. It can be used for inhibiting
XX leukocyte infiltration of tissues, e.g. for treating inflammatory
XX diseases such as inflammatory bowel disease. The immunoglobulin can
XX also be used for detection, isolation and diagnosis.
XX
XX Sequence 112 AA;
XX
XX Query Match 100.0%; Score 695; DB 19; Length 132;
XX Best Local Similarity 100.0%; Pred. No. 3e-48;
XX Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKLPVRLVLLFWIPVSGGDVVVTQTPLSPVSGDQVSISCRSSQSLAKSYGNTYLSW 60
DB 1 mklpvrllvlllfpvsggdvvvtqtplslpvsfgdqvsiscrssqslaksygnlyslw 60
QY 61 YLHKPGQSPQLLIYIGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOGTHQP 120
DB 61 ylhkpggspqlliyigisnrfsgvdpdrfsgsggtdtflkistikpedlgmyyclgqthqp 120
QY 121 YTFGGGKLEIK 132
DB 121 ytfgggkkleik 132
XX
RESULT 2
W53817
ID W53817 standard; Protein; 140 AA.
XX
AC W53817;
XX
XX 14-JUL-1998 (first entry)
XX
XX Consensus protein sequence of the murine variable light chain region.
XX
XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
XX Muscosal adressin cell adhesion molecule-1; MacCAM-1;
XX humanised antibody; murine antigen binding region; inhibition;
XX leukocyte infiltration of tissue; treatment; inflammatory disease;
XX inflammatory bowel disease.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..20 /note= "signal peptide"
XX Protein 21..140 /note= "mature protein"
XX
XX W09806248-A:.
XX
XX 19-FEB-1998
XX
XX 06-AUG-1997 97WO-US13884.

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XX 15-AUG-1996; 96US-0700737.
XX (LEUK-) LEUKOSITE INC.
XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
XX Saldanha J;
XX WPI: 1998-159172/14.
XX N-PSDB: V20086.
XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
XX used for treating inflammatory disease, pancreatitis, diabetes,
XX asthma, graft versus host disease and sarcoidosis
XX
XX Example 1; Fig 3; 145pp; English.
XX
XX The present sequence represents the consensus amino acid sequence
XX comprising the variable region of murine Act-1 antibody determined from
XX several independent mouse light chain variable region clones. Act-1 is
XX active against human alpha4-beta7 integrin. Muscosal adressin cell
XX adhesion molecule-1 (MacCAM-1) is a ligand of this particular integrin.
XX The Act-1 antibody interferes with alpha4-beta7 integrin binding to
XX MacCAM-1, which is present of high endothelial venules in mucosal
XX lymph nodes. Variable regions were amplified from DNA encoding Act-1
XX using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
XX produced several different sequences, of which the present sequence is a
XX consensus sequence. The present sequence was used to construct
XX chimeric, humanised Act-1 antibodies, which contain murine antigen
XX binding regions. The humanised immunoglobulin can be used to inhibit
XX the interaction of cells bearing alpha4-beta7 with cells bearing a
XX ligand for alpha4-beta7. It can be used for inhibiting leukocyte
XX infiltration of tissues, e.g. for treating inflammatory diseases such
XX as inflammatory bowel disease. The immunoglobulin can also be used for
XX detection, isolation and diagnosis.
XX
XX Sequence 140 AA;
XX
XX Query Match 100.0%; Score 695; DB 19; Length 140;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-48;
XX Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKLPVRLVLLFWIPVSGGDVVVTQTPLSPVSGDQVSISCRSSQSLAKSYGNTYLSW 60
DB 1 mklpvrllvlllfpvsggdvvvtqtplslpvsfgdqvsiscrssqslaksygnlyslw 60
QY 61 YLHKPGQSPQLLIYIGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOGTHQP 120
DB 61 ylhkpggspqlliyigisnrfsgvdpdrfsgsggtdtflkistikpedlgmyyclgqthqp 120
QY 121 YTFGGGKLEIK 132
DB 121 ytfgggkkleik 132
XX
RESULT 3
W53812
ID W53812 standard; Protein; 138 AA.
XX
AC W53812;
XX
XX 14-JUL-1998 (first entry)
XX
XX Light chain of a humanised murine Act-1 antibody.
XX
XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
XX Muscosal adressin cell adhesion molecule-1; MacCAM-1;
XX humanised antibody; murine antigen binding region; inhibition;
XX leukocyte infiltration of tissue; treatment; inflammatory disease;
XX inflammatory bowel disease.
XX
XX Synthetic.
XX
OS

```

OS Mus sp.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /note= "signal peptide"
 FT 21..138
 FT /note= "mature protein"
 XX
 XX W09806248-A2.
 XX
 XX 19-FEB-1998.
 XX
 XX 06-AUG-1997; 97WO-US13884.
 XX
 XX 15-AUG-1996; 96US-0700737.
 XX
 XX (LEUK-) LEUKOSITE INC.
 XX
 XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX
 XX WPI: 1998-159172/14.
 DR N-PSDB; V20075.
 XX
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX
 XX Claim 15; Fig 12; 145pp; English.
 XX
 XX The present sequence represents the light chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MacCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 XX
 SQ Sequence 138 AA;
 Query Match 87.5%; Score 608; DB 19; Length 138;
 Best Local Similarity 87.1%; Pred. No. 2.4e-41;
 Matches 115; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLLFWIPVSGGDDVVTQTPLSLPVSGDQVSISSRSSQSLAKSYGNTYLSW 60
 DB 1 mkplrvllvlwlpvsggddvmtqspislptpggepasiscrssqslaksygntylsw 60
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLOGTHQP 120
 DB 61 ylkpgsqpqllygisnrfsgvdpdrfsgsgsgtdftlkisrveaedgvyyclqgthqp 120
 QY 121 YTFGGGKLEIK 132
 DB 121 ytfgggkveik 132
 RESULT 4
 W14942
 ID W14942 standard; Protein; 238 AA.
 XX
 AC W14942;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE 3F4 Human IgG4 expression plasmid insert product (light chain).
 XX

KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 OS Mus sp.
 XX WO9711971-A1.
 PN 03-APR-1997.
 PD 27-SEP-1996; 96WO-US15575.
 PF 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX (ALEX-) ALEXION PHARM INC.
 XX Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX WPI: 1997-212855/19.
 DR N-PSDB; T62938.
 XX
 XX Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 65-66; 105pp; English.
 XX
 XX Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W14937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 XX
 SQ Sequence 238 AA;
 Query Match 80.5%; Score 559.5; DB 18; Length 238;
 Best Local Similarity 81.1%; Pred. No. 3e-37;
 Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFWIPVSGGDDVVTQTPLSLPVSGDQVSISSRSSQSLAKSYGNTYLSW 60
 DB 1 mkplrvllvlwlpvsggddvmtqspislptpggepasiscrssqslvhsngntylqw 59
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLOGTHQP 120
 DB 60 ylkpgsqpqllygisnrfsgvdpdrfsgsgsgtdftlkisrveaedlgyvfcsqstchp 119
 QY 121 YTFGGGKLEIK 132
 DB 120 ftfgggkkleik 131
 RESULT 5
 W14937
 ID W14937 standard; Protein; 238 AA.
 XX
 AC W14937;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE Murine anti-porcine VCAM 3F4 light chain.
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX

[illegible]

CC	GD2-specific cells (cellular response). It can be used to purify
CC	anti-IA7 (Ab3), anti-GD2 (Ab1') or 14G2a (Ab1), detect anti-IA7 or
CC	anti-GD2 in a sample or measure the level of cellular anti-IA7 or
CC	anti-GD2 activity.
CC	The cDNA can be used in expression systems for IA7 prodn., and in
CC	the prepn. of probes and primers to respectively assay for IA7
CC	cDNA, and amplify desired polynucleotides for use in gene therapy.
XX	
SQ	Sequence 149 AA;
	Query Match 79.8%; Score 554.5; DB 17; Length 149;
	Best Local Similarity 79.5%; Pred. NO. 4.6e-37;
	Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps
OY	1 MKLIPVRLLLFPIPVSGDDVVVTQLPLSPVFGDQVSISCRSSQSLAKSYGNTYLSW 60
Db	: :: :
	1 mklipvrlly-lmfwpasddvltmtqplslpvsldgasiscraqsqivhangntylew 59
OY	61 YLHKPGSQPOLLYGISNRFSGVPDRFSGSGCTDTFLKISTIKPEDLCMYVCLOGTHOP 120
Db	
	60 Ylqkpgsqpnlllyfnsrnfsgvpdrfsgsggtdftlkisrveadlgvyvcfgshyp 119
OY	121 YTFGGGTKLEIK 132
Db	:
	120 wtfgggtkleik 131
RESULT	8
ID	Y2I545
ID	Y2I545 standard; Protein; 149 AA.
XX	
AC	Y2I545;
DT	
DT	03-AUG-1999 (first entry)
XX	
DE	Monoclonal antibody IA7 light chain variable region.
XX	
KW	Psoriasis; immunological response; anti-idiotypic antibody; glutamate;
KW	chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;
KW	monoclonal antibody; IA7.
OS	Unidentified.
XX	
PN	WO925380-A2.
PD	27-MAY-1999.
PF	17-NOV-1998; 98WO-US24607.
XX	
PR	16-NOV-1998; 98US-0192838.
PR	17-NOV-1997; 97US-006577A.
XX	
PPA	(KENT) UNIV KENTUCKY RES FOUND.
XX	
PI	Chatterjee M, Foon KA;
XX	
XX	WPI: 1999-347407/29.
DDR	N-PSDB; X60629.
XX	
TPT	Treatment of psoriasis
XX	
XX	Disclosure; Fig 2; 48pp; English.
XX	
CCC	The invention provides a method of treating of psoriasis by administer-
CCC	an antigen which has similar immunogenic properties to an antigen
CCC	expressed on cells of psoriatic tissue so that an immunological respon-
CCC	is elicited in the individual. The antigen stimulates the generation o
CCC	anti-idiotypic antibodies that neutralize the aberrant immune response
CCC	causing the psoriasis. The method is used to treat psoriasis, especial
CCC	chronic plaque, guttate, pustular, plaque-type psoriasis or psoriatic
CCC	arthritis. The compositions allow the individual's own immune system t
CCC	act against psoriatic tissue. The present sequence represents the ligand
CCC	


```
XX 26-MAY-1994.
PD
XX 15-NOV-1993; 93WO-US11316.
PF
XX 13-NOV-1992; 92US-0977706.
PR
XX 13-NOV-1992; 92US-0977707.
PR
XX 28-SEP-1993; 93US-0128015.
PR
XX (CANC-) CANCER RES FUND CONTRA COSTA.
PA
XX WPI: 1994-183509/22.
XX N-PSDB; Q62763.
XX Chimeric human-murine polypeptide(s) specific for human mammary
PT fat globule antigen - for imaging, diagnosing and treating
PT neoplasia, with less undesirable immunogenic response
XX
XX Example 27; Page 41; 54pp; English.
XX An initial isolation of cDNAs coding for murine anti-human breast
CC carcinoma MAb KC-4 was performed using PCR with commercially
CC available primers (see Q62751-Q62758, available from NOVAGEN).
CC Subsequent cloning using PCR primers JO20, JO21, JO22 and JO24
CC (see Q62759-Q62762) resulted in the isolation of the mouse Ig
CC variable domains. The amplified cDNAs were sequenced (Q62763 and
CC Q62764) and amino acid sequences were deduced from them. Chimeric
CC mouse-human antibodies were constructed using human constant
CC regions so as to produce less immunogenic polypeptides which
CC retained the anti-human carcinoma binding specificity of KC-4.
XX
XX Sequence 131 AA;
SQ
Query Match 78.9%; Score 548.5; DB 15; Length 131;
Best Local Similarity 78.8%; Pred. NO. 1.2e-36;
Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLLEWIPVSGGDVVVTOTPLSLPVSGDOVSICRSQSOLAKSYGNTYLSW 60
DB 1 mklpvrllv-lmfwipassdvltqtplslpvsgdqasiscrsqsvhsgntylew 59
QY 61 YLHKPGQSPOLLYIGISNRFSGSGGTDFTLKISTIKPEDLGMYYCLQGTQHP 120
DB 60 ylkpgqgspkillykvsirfsgsgsgtdftlnlsrveaedlglyycfggshvp 119
QY 121 YTFGGGTGLEIK 132
DB 120 ytfgggtgleik 131
RESULT 13
ID R52790 standard; Protein; 131 AA.
AC AC
XX R52790;
XX
XX 24-JAN-1995 (first entry)
XX Murine KC-4 immunoglobulin light chain variable region (deduced).
XX Immunoglobulin variable domain; primer; polymerase chain reaction;
KW chimeric antibody; human milk fat globule; human breast carcinoma;
KW murine anti-human carcinoma monoclonal antibody KC-4.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Protein 20..131
XX /label= KC-4_mature_VL-chain
XX Region 20..42
XX /label= FR1
XX Region 43..58
FT
```

```
FT Region /label= CDR1
FT 59..73
FT /label= FR2
FT 74..80
FT /label= CDR2
FT 81..112
FT /label= FR3
FT 98..100
FT /note= "putative glycosylation site"
FT 113..121
FT /label= CDR3
FT 122..131
FT /label= FR4
XX
XX WO9411509-A.
XX
XX 26-MAY-1994.
XX
XX 16-NOV-1993; 93WO-US11445.
XX
XX 16-NOV-1992; 92US-0977696.
XX 30-SEP-1993; 93US-0129930.
XX 08-OCT-1993; 93US-0134346.
XX
XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX
XX Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
XX WPI: 1994-183510/22.
XX New analogue peptide(s) comprising antibody variable regions -
XX used to develop prods. for use in the detection, diagnosis,
XX therapy and prevention of neoplasms
XX
XX Example 26; Page 61; 109pp; English.
XX
XX An initial isolation of cDNAs coding for murine anti-human breast
CC carcinoma MAb KC-4 was performed using PCR with commercially
CC available primers (see Q62776-Q62783, available from NOVAGEN).
CC Subsequent cloning using PCR primers JO20, JO21, JO22 and JO24
CC (see Q62784-Q62787) resulted in the isolation of the mouse Ig
CC variable domains. The amplified cDNAs were sequenced (Q62788 and
CC Q62789) and amino acid sequences were deduced from them. Chimeric
CC mouse-human antibodies were constructed using human constant
CC regions so as to produce less immunogenic polypeptides which
CC retained the anti-human carcinoma binding specificity of KC-4.
XX
XX Sequence 131 AA;
SQ
Query Match 78.9%; Score 548.5; DB 15; Length 131;
Best Local Similarity 78.8%; Pred. NO. 1.2e-36;
Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLLEWIPVSGGDVVVTOTPLSLPVSGDOVSICRSQSOLAKSYGNTYLSW 60
DB 1 mklpvrllv-lmfwipassdvltqtplslpvsgdqasiscrsqsvhsgntylew 59
QY 61 YLHKPGQSPOLLYIGISNRFSGSGGTDFTLKISTIKPEDLGMYYCLQGTQHP 120
DB 60 ylkpgqgspkillykvsirfsgsgsgtdftlnlsrveaedlglyycfggshvp 119
QY 121 YTFGGGTGLEIK 132
DB 120 ytfgggtgleik 131
RESULT 14
ID R70457 standard; Peptide; 131 AA.
XX AC
XX R70457;
XX
```

DT 27-OCT-1995 (first entry)
 XX VL sequence of anti-KC-4 monoclonal antibody (kII-Jk2).
 DE Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.
 XX Synthetic.
 KW WO9510776-A.
 OS 20-APR-1995.
 PN 16-NOV-1993; 93WO-US11444.
 PD 08-OCT-1993; 93US-0134346.
 XX (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
 XX Ceriani RL, Docouto JJR, Peterson JA;
 PI WPI; 1995-161912/21.
 DR N-PSDB; Q87531.
 XX New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells, in vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PT Example; Table 14, Page 31; 61pp; English.
 PS The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL
 XX were prepared by PCR from polyadenylated RNA isolated from 100
 CC million KC-4 hybridoma cells. All clones were obtd. from independent
 CC PCRs. The sequences of the primers are given in Q87519-Q87526.
 CC The PCR products were cloned, without prior purification, into pCR1000
 CC (Invitrogen) and sequenced in both directions. The VL DNA sequence and
 CC its derived protein sequences are shown in Q87531 and R70449-R70457.
 CC The mature VL chain begins at AA D of framework 1 (FR1). VL is a
 CC group II kappa chain. Part of the CDR3 and all of the FR4 are
 CC encoded by Jk2. There is an asparagine glycosylation site in the
 CC light chain in FR3. The site reads NIS. R70457 is a composite
 CC sequence of R70449-R70456.
 XX Sequence 131 AA;

Query Match 78.9%; Score 548.5; DB 16; Length 131;
 Best Local Similarity 78.8%; Pred. No. 1.2e-36;
 Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 mklpvrllv-lmfwpasssdvmtqtplslpvsigdqasiscrssqslvhsngntylew 59
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGGTFTLTIKSTIKPEDLGMYYCLQGTHQP 120
 DB 60 ylkpgsqpklilykvsirfsgvdpdrfsgsggtftltikstikrveadlgyycfcgshvp 119
 QY 121 YTFGGGTTKLEIK 132
 DB 120 ytfggggtkleik 131

RESULT 15
 Y17416
 ID Y17416 standard; Protein; 238 AA.
 AC Y17416;
 XX 26-JUL-1999 (first entry)
 DT Mouse immunoglobulin E light chain.
 DE Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
 KW

XX Mus sp.
 OS Key
 XX Location/Qualifiers
 FH 1..19
 FT Peptide
 FT /label= signal
 FT 20..238
 FT /label= immunoglobulin_E_light_chain
 XX EP921189-A1.
 PN 09-JUN-1999.
 PD 13-NOV-1998; 98EP-0309340.
 XX 14-NOV-1997; 97JP-0313989.
 PR (SANY) SANKYO CO LTD.
 PA (TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
 XX Karasuyama H, Matsuoka K, Taya C, Yonemawa H;
 PI WPI; 1999-315404/27.
 DR N-PSDB; X61085.
 XX Transgenic non-human animal allergy models
 PT Claim 28; Page 30-32; 42pp; English.
 PS The present invention describes a transgenic, non-human animal with its
 CC genome altered to constitutively express a molecule having a constant
 CC region which can bind an IgE receptor on mast cells in the animals, the
 CC molecule having an immunoglobulin structure and being further capable of
 CC specifically binding a predetermined antigen. The transgenic animal is
 CC useful as a model for evaluating the activity and the ability of
 CC substances i.e. with anti-allergic activity, to affect any allergic
 CC reaction caused in the animal by the administration of the antigen to
 CC the animal, and applying the substance to be evaluated. The present
 CC sequence is the mouse immunoglobulin E (IgE) light chain, given in
 CC the present invention.
 XX Sequence 238 AA;

Query Match 78.6%; Score 546.5; DB 20; Length 238;
 Best Local Similarity 78.0%; Pred. No. 3.2e-36;
 Matches 103; Conservative 11; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 mklpvrllv-lmfwpasssdvmtqtplslpvsigdqasiscrssqslvhsngntylew 59
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGGTFTLTIKSTIKPEDLGMYYCLQGTHQP 120
 DB 60 ylkpgsqpklilykvsirfsgvdpdrfsgsggtftltikstikrveadlgyycfcgshvp 119
 QY 121 YTFGGGTTKLEIK 132
 DB 120 ltfggggtkleik 131

Search completed: April 13, 2001, 15:35:39
 Job time: 118 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:55 ; Search time 4.45 Seconds
(without alignments)
51.491 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLLEWIPVSGG.....CLOGTHQPTFGGKTLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7695 seqs, 1735856 residues

Total number of hits satisfying chosen parameters: 7695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pap:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pap:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pap:*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	391.5	56.3	240	5	US-09-782-504-4
2	366.5	52.7	495	5	US-09-509-031-4
3	357.5	51.4	482	5	US-09-509-031-16
4	334.5	51.0	155	5	US-09-509-031-11
5	334.5	51.0	342	5	US-09-509-031-6
6	304	43.7	128	4	US-08-475-815A-7
7	303.5	43.7	109	5	US-09-386-658-4
8	101	14.5	140	4	US-08-475-815A-11
9	90.5	13.0	132	5	US-09-386-658-2
10	74	10.6	582	5	US-09-533-077-334
11	70.5	10.1	640	5	US-09-808-689-12
12	69.5	10.0	342	5	US-09-815-108-20
13	69.5	10.0	509	5	US-09-815-108-3
14	69.5	10.0	529	5	US-09-815-108-2
15	69.5	10.0	594	5	US-09-815-108-22
16	67.5	9.7	478	5	US-09-815-108-6
17	67.5	9.7	472	5	US-09-815-108-5
18	67.5	9.7	504	5	US-09-815-108-8
19	67.5	9.7	504	5	US-09-815-108-15
20	67.5	9.7	504	5	US-09-815-108-17
21	67.5	9.7	504	5	US-09-815-108-19
22	65	9.4	299	5	US-09-808-689-6
23	62.5	9.0	331	6	US-60-278-037-2
24	62.5	9.0	740	1	PCT-US01-09226-61
25	62.5	9.0	1250	1	PCT-US01-09226-62
26	62	8.9	312	5	US-09-808-689-2
27	61.5	8.8	2399	5	US-09-739-449-11472

28	60	8.6	680	5	US-09-739-449-11753	Sequence 11753, A
29	58	8.3	304	5	US-09-739-449-9355	Sequence 9355, Ap
30	57.5	8.3	209	5	US-09-739-449-11033	Sequence 11033, A
31	57.5	8.3	325	5	US-09-739-449-8751	Sequence 8751, Ap
32	57.5	8.3	574	5	US-09-815-108-7	Sequence 7, Appl
33	57	8.2	868	5	US-09-739-449-12606	Sequence 12606, A
34	56.5	8.1	427	5	US-09-739-449-10896	Sequence 10896, A
35	56.5	8.1	546	5	US-09-739-449-12091	Sequence 12091, A
36	56	8.1	550	5	US-09-739-449-9798	Sequence 9798, Ap
37	56	8.1	654	6	US-60-278-037-7	Sequence 7, Appl
38	55.5	8.0	1085	5	US-09-739-449-9734	Sequence 9734, Ap
39	55	7.9	299	5	US-09-809-391-396	Sequence 396, App
40	55	7.9	490	5	US-09-739-449-13176	Sequence 13176, A
41	54.5	7.8	176	5	US-09-739-449-10487	Sequence 10487, A
42	54	7.8	118	5	US-09-739-449-11965	Sequence 11965, A
43	54	7.8	385	5	US-09-739-449-9552	Sequence 9552, Ap
44	54	7.8	1059	5	US-09-808-689-10	Sequence 10, Appl
45	54	7.8	1119	5	US-09-808-689-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-782-504-4
; Sequence 4, Application US/09782504
; GENERAL INFORMATION:
; APPLICANT: Hellstrom, Ingegerd
; Bruce, Kim Folger
; Schreiber, George J.
; Siegall, Clay
; McAndrew, Stephen
; TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN
; CARCINOMAS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,504
; FILING DATE: 12-Feb-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 840065.405D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-782-504-4

Query Match 56.3%; Score 391.5; DB 5; Length 240;
Best Local Similarity 70.6%; Pred. No. 9.1e-34;
Matches 84; Conservative 10; Mismatches 16; Indels 9; Gaps 6;

Query Match	51.0%;	Score 354.5;	DB 5;	Length 342;
Best Local Similarity	61.9%;	Pred. No. 7.8e-30;		


```

Db      55  HWFOQKSGSPKWIYATSNLASGVPVRFSGSGSGTYSLTISRVEDAATYCOOWTS 114
Qy      119  QPYTFGGGTKLEIK 132
           | | | | | | | | | |
Db      115  NPPTFGGGTKLEIK 128

RESULT  7
US-09-386-658-4
; GENERAL INFORMATION:
; APPLICANT: Erlanger, Bernard
; APPLICANT: Chen, Bi-Xing
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
; FILE REFERENCE: 0575-54182/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/386,658
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-09-386-658-4

Query Match 43.7%; Score 303.5; DB 5; Length 109;
Best Local Similarity 52.7%; Pred.No.3e-25;
Matches 59; Conservative 19; Mismatches 29; Indels 5; Gaps

Qy      21  DVVVQTPLSLPVSFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPQSQPLLIIYGISNRF 80
           | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  DIQMTTSSLSASLGRVTFSCASQDI-----NNYLNWYQQKPDGTTIKLLIYYTSSLR 55

Qy      81  SGVYDFRFGSGSGGDTFLKISITIKPEDLGMYYCLQTHOPYTFGGGTKLEIK 132
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      56  SGVPSRFSGSGSGTGYSLTNINLEPDATYFCQQYSRLPFTFGSGTKLEIK 107

RESULT  8
US-08-475-815A-11
; Sequence 11, Application US/08475815A
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RES
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B C
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 23522-0157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-815A-11

Query Match 14.5%; Score 101.; DB 4; Length 140;
Best Local Similarity 26.4%; Pred. No. 0.00014;
Matches 34; Conservative 26; Mismatches 47; Indels 22; Gaps 7;

QY 9 VLLFLWIPVSGGVVVTQTPLSLP----VSFGDQVSISSCRSSQSLAKSYGNTYLSWYLHK 64
Db 5 LILLFLVAVA--TFVLQVQLQOPGAELVKPGASVKMSCKASGVTFTSYN---MHWVKQT 59

QY 65 PGQSPQL--IY-----GTSNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQG 116
Db 60 PGRGLEV IGAIYPGNGDTSYNOKFKGKATLTADKSSSTAY-MQLSSLTSDSAVYYCARS 118

QY 117 THQPYTIGG 125
Db 119 TY-----YGG 123

RESULT 9
US-09-386-658-2
; Sequence 2, Application US/09386658
; GENERAL INFORMATION:
; APPLICANT: Erlander, Bernard
; APPLICANT: Chen, Bi-Xing
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
; FILE REFERENCE: 0575-54182/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/386,658
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: mouse [murine]
US-09-386-658-2

Query Match 13.0%; Score 90.5; DB 5; Length 132;
Best Local Similarity 25.0%; Pred. No. 0.0015;
Matches 33; Conservative 31; Mismatches 49; Indels 19; Gaps 8;

QY 11 LLEWIPVSGG---DVVVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWYLHKPGQ 67
Db 7 MLFLLSITAGVHCQVHLOQSGPEL--VRPGASVKISCKTSGVY---FSSSWNNWVKQRPQ 62

QY 68 SPQLL--IY-----GTSNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQGTQH 119
Db 63 GLKWTIG IYPGNGNTNYNEKFKGKATLTADKSSNTAY-MQLSSLTSDSAVYFC--ATSS 119

QY 120 PYTFGGYTKLEI 131
Db 120 AY-WQQYITLTV 130

RESULT 10
US-09-533-077-334
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```
; Sequence 334, Application US/09533077
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C5
; CURRENT APPLICATION NUMBER: US/09/533,077
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 800
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-077-334

Query Match 10.6%; Score 74; DB 5; Length 582;
Best Local Similarity 22.0%; Pred. No. 0.42;
Matches 27; Conservative 15; Mismatches 49; Indels 32; Gaps 4;

QY 6 RLLVLLLF-----WLPVSGGVVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGN 55
Db 9 RLLFCLLISATVFRPGLGWTVNS-----AYGDTIIIPCRLDVDPQNLNMF- 53

QY 56 TYLSWYLHRPQSPOLLIIYISNR---PSGVDPDRFSGSGGTDFTLKISTIKPEDLGMV 111
Db 54 ---KWYKPEKPGSPVFIAPRSSTKKSQVQDDVPEYKDRNLNSENLYLSISNARISDEKRF 110

QY 112 YCL 114
Db 111 VCM 113

RESULT 11
US-09-808-689-12
; Sequence 12, Application US/09808689
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Audrey Goddard
; APPLICANT: Gurney, Austin L.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1624R2C1
; CURRENT APPLICATION NUMBER: US/09/808,689
; CURRENT FILING DATE: 2001-03-14
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 12
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-689-12

Query Match 10.1%; Score 70.5; DB 5; Length 640;
Best Local Similarity 25.0%; Pred. No. 1.1;
Matches 23; Conservative 15; Mismatches 35; Indels 19; Gaps 3;

QY 23 VVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWYLHKPQSPOLLIIYISNRFSG 82
Db 355 VIVEPPADLNVTGMAAEKLCRASTSL-----TSVSWIT-----PNCVTMTHGAYKVRIA 404

QY 83 VPDRFSGSGGTDFTLKISTIKPEDLGMVYCL 114
Db 405 VL-----SDGTLNFTNVTQDTGMTCM 427
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```
RESULT 12
US-09-815-108-20
; Sequence 20, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-815-108-20

Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 342;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 23 VVTQT-PLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQSPOLLIYGISNRFS 81
DB 217 VLTGTHPVNTTDFGTTTSFQCK-----VRSDVKPVIQWL-----KRVEYSGEGRHN 263
QY 82 GVDP-----RFGSGSGTDTFT-----LKISTIKPEDLGMYYCLOGTHQHPYTF 123
DB 264 STIDVGGQKFVVLPTGDMVSRPDGSGYLNKLISRARQDDAGMYICLGANTMGYSF 318

RESULT 13
US-09-815-108-3
; Sequence 3, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (355)..(375)
US-09-815-108-3

Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 509;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 23 VVTQT-PLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQSPOLLIYGISNRFS 81
DB 223 VLTGTHPVNTTDFGTTTSFQCK-----VRSDVKPVIQWL-----KRVEYSGEGRHN 269
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QY 82 GVDP-----RFGSGSGTDTFT-----LKISTIKPEDLGMYYCLOGTHQHPYTF 123
DB 270 STIDVGGQKFVVLPTGDMVSRPDGSGYLNKLISRARQDDAGMYICLGANTMGYSF 324

RESULT 14
US-09-815-108-2
; Sequence 2, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-815-108-2
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Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 529;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 23 VVTQT-PLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQSPOLLIYGISNRFS 81
DB 243 VLTGTHPVNTTDFGTTTSFQCK-----VRSDVKPVIQWL-----KRVEYSGEGRHN 289
QY 82 GVDP-----RFGSGSGTDTFT-----LKISTIKPEDLGMYYCLOGTHQHPYTF 123
DB 290 STIDVGGQKFVVLPTGDMVSRPDGSGYLNKLISRARQDDAGMYICLGANTMGYSF 344
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RESULT 15
US-09-815-108-22
; Sequence 22, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine FGFR-L
; OTHER INFORMATION: extracellular domain-Fc fusion polypeptide
US-09-815-108-22

Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 594;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:47 ; Search time 117.03 seconds
(without alignments)
181.430 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLQGTHTQPTFGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

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3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	695	100.0	132	11 US-08-700-737-12	Sequence 12, Appl
2	695	100.0	140	11 US-08-700-737-6	Sequence 6, Appl
3	616	88.6	138	11 US-08-700-737-21	Sequence 21, Appl
4	593	85.3	112	11 US-08-700-737-7	Sequence 7, Appl
5	554.5	79.8	149	15 US-09-192-838-2	Sequence 2, Appl
6	554.5	79.8	149	17 US-09-324-191-2	Sequence 2, Appl
7	552.5	79.5	149	16 US-09-293-533-2	Sequence 2, Appl
8	550.5	79.2	131	19 US-09-523-095A-6	Sequence 6, Appl
9	537.5	77.3	131	5 US-08-134-346A-50	Sequence 50, Appl
10	537.5	77.3	131	13 US-08-976-288A-95	Sequence 95, Appl

11 536.5 77.2 131 8 US-08-485-044-4 Sequence 4, Appl
12 535.5 77.1 238 12 US-08-827-223-10 Sequence 10, Appl
13 535.5 77.1 238 12 US-08-827-223-10 Sequence 10, Appl
14 535.5 77.1 238 14 US-09-046-351-10 Sequence 10, Appl
15 530.5 76.3 131 19 US-09-523-095A-10 Sequence 10, Appl
16 527.5 75.9 173 3 US-07-946-313-3 Sequence 3, Appl
17 527.5 75.9 173 3 US-07-946-314-3 Sequence 3, Appl
18 527.5 75.9 173 10 US-08-650-108-3 Sequence 3, Appl
19 523.5 75.3 149 14 US-09-059-063-9 Sequence 9, Appl
20 519.5 74.7 131 3 US-07-977-706A-11 Sequence 11, Appl
21 519.5 74.7 131 3 US-07-977-706C-11 Sequence 11, Appl
22 519.5 74.7 131 3 US-07-977-707B-11 Sequence 11, Appl
23 519.5 74.7 131 5 US-08-128-015-11 Sequence 11, Appl
24 519.5 74.7 131 13 US-08-976-288A-11 Sequence 11, Appl
25 514 74.0 112 11 US-08-700-737-52 Sequence 52, Appl
26 513 73.8 127 6 US-08-286-754-45 Sequence 45, Appl
27 513 73.8 127 8 US-08-408-724-45 Sequence 45, Appl
28 513 73.8 127 8 US-08-472-819-45 Sequence 45, Appl
29 513 73.8 127 8 US-08-487-113C-45 Sequence 45, Appl
30 513 73.8 127 17 US-09-350-273-45 Sequence 45, Appl
31 513 73.8 127 17 US-09-382-289-45 Sequence 45, Appl
32 513 73.8 127 21 US-09-753-436-45 Sequence 45, Appl
33 503 72.4 239 14 US-09-046-351-78 Sequence 78, Appl
34 503 72.4 239 14 US-09-046-351-82 Sequence 82, Appl
35 500 71.9 129 12 US-08-827-223-82 Sequence 82, Appl
36 499 71.8 239 14 US-09-046-351-80 Sequence 80, Appl
37 499 71.8 239 14 US-09-046-351-84 Sequence 84, Appl
38 492.5 70.9 113 11 US-08-700-737-50 Sequence 50, Appl
39 492 70.8 263 16 US-09-293-533-66 Sequence 66, Appl
40 492 70.8 285 17 US-09-318-661-4 Sequence 4, Appl
41 488.5 70.3 219 5 US-08-155-874B-60 Sequence 60, Appl
42 488.5 70.3 219 10 US-08-665-839A-60 Sequence 60, Appl
43 488.5 70.3 219 10 US-08-665-839A-60 Sequence 60, Appl
44 488.5 70.3 219 10 US-08-665-839B-60 Sequence 60, Appl
45 488 70.2 219 18 US-09-454-925A-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-700-737-12
: Sequence 12, Application US/08700737
: GENERAL INFORMATION:
: APPLICANT: Ponath, Paul D.
: APPLICANT: Ringler, Douglas J.
: APPLICANT: Jones, S. Tarran
: APPLICANT: Newman, Walter
: APPLICANT: Saldanha, Jos
: APPLICANT: Bendig, Mary M.
: TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
: TITLE OF INVENTION: INTEGRIN
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/700,737
: FILING DATE: 15-AUG-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: LKS95-10

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-700-737-12

Query Match 100.0%; Score 695; DB 11; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.3e-61;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMYYCLOGTHOP 120
DB 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMYYCLOGTHOP 120
QY 121 YTFGGGTRLEIK 132
DB 121 YTFGGGTRLEIK 132

RESULT 2
US-08-700-737-6
Sequence 6, Application US/08700737
GENERAL INFORMATION:
APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700.737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-700-737-6

Query Match 100.0%; Score 695; DB 11; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMYYCLOGTHOP 120
DB 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMYYCLOGTHOP 120
QY 121 YTFGGGTRLEIK 132
DB 121 YTFGGGTRLEIK 132

RESULT 3
US-08-700-737-21
Sequence 21, Application US/08700737
GENERAL INFORMATION:
APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700.737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-700-737-21

Query Match 88.6%; Score 616; DB 11; Length 138;
Best Local Similarity 87.9%; Pred. No. 2.4e-53;
Matches 116; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSIICRSQSLAKSYGNTYLSW 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMYYCLOGTHOP 120
DB 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMYYCLOGTHOP 120

Db 61 YLQKPGSQPLLIIYGISNRFSGVDPDRFSGSGCTDTFLKISRVEADGVVYICLQGTQHP 120
QY 121 YTFGGGTTKLEIK 132
Db 121 YTFGGGTTKLEIK 132
RESULT 4
US-08-700-737-7
; Sequence 7, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; TITLE OF INVENTION: INTEGRIN
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-700-737-7

Query Match 85.3%; Score 593; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 DVVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWLHKPGSQPLLIIYGISNRF 80
Db 1 DVVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWLHKPGSQPLLIIYGISNRF 60
QY 81 SCVDPDRFSGSGCTDTFLKISTIRPEDLGMYCYCLOGTQHPYTFGGGTTKLEIK 132
Db 61 SCVDPDRFSGSGCTDTFLKISTIRPEDLGMYCYCLOGTQHPYTFGGGTTKLEIK 112
RESULT 5
US-09-192-838-2
; Sequence 2, Application US/09192838
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000500

; CURRENT APPLICATION NUMBER: US/09/192,838
; CURRENT FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-192-838-2

Query Match 79.8%; Score 554.5; DB 15; Length 149;
Best Local Similarity 79.5%; Pred. No. 3.2e-47;
Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLLFWIPVSGDQVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFWIPASSDDVLMQTPLSLPVSGLDQASISCRSSQSIHVSNGNTYLEW 59
QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGCTDTFLKISTIRVEADLGMYCYCLOGTQHP 120
Db 60 YLQKPGSQPNLLIYFVSNRFSQVDPDRFSGSGCTDTFLKISRVEADLGMYCYCLOGSHVP 119
QY 121 YTFGGGTTKLEIK 132
Db 120 WTFGGGTTKLEIK 131
RESULT 6
US-09-324-191-2
; Sequence 2, Application US/09324191
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
; APPLICANT: CHATTERJEE, Malaya
; APPLICANT: FOON, Kenneth A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000540
; CURRENT APPLICATION NUMBER: US/09/324,191
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: 60/065,774
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-324-191-2

Query Match 79.8%; Score 554.5; DB 17; Length 149;
Best Local Similarity 79.5%; Pred. No. 3.2e-47;
Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLLFWIPVSGDQVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFWIPASSDDVLMQTPLSLPVSGLDQASISCRSSQSIHVSNGNTYLEW 59
QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGCTDTFLKISTIRVEADLGMYCYCLOGTQHP 120
Db 60 YLQKPGSQPNLLIYFVSNRFSQVDPDRFSGSGCTDTFLKISRVEADLGMYCYCLOGSHVP 119
QY 121 YTFGGGTTKLEIK 132
Db 120 WTFGGGTTKLEIK 131
RESULT 7
US-09-293-533-2
; Sequence 2, Application US/09293533
; GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya
APPLICANT: Moon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 735 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-293-533-2

Query Match 79.5%; Score 552.5; DB 16; Length 149;
Best Local Similarity 79.5%; Pred. No. 5.1e-47;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTOTPLSLPVSGDQVSIQSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFVIPASSDDVFMOTPLSLPVSLGDAQSISCRSSQSLVHSNGNTYLEW 59
QY 61 YLHKPGKSPQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYCLOGTHQP 120
DB 60 YLQKPGKSPNLLIYFVSNRFSGVDPDRFSGSGGTDTFLKISRVEAEDLGYYVCFQGSHPV 119
QY 121 YTFGGGKLEIK 132
DB 120 WTFGGGKLEIK 131

RESULT 8
US-09-523-095A-6
Sequence 6, Application US/09523095A
GENERAL INFORMATION:
APPLICANT: FUKUSHIMA, Naoshi
APPLICANT: FUKUSHIMA, Shinsuke
APPLICANT: OHI-EDA, Masayoshi
APPLICANT: KUCHI, Yasufumi
TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV
FILE REFERENCE: 065678/0102
CURRENT APPLICATION NUMBER: US/09/523,095A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: JP 11-63557
PRIOR FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 131
TYPE: PRT
ORGANISM: Mus sp.
US-09-523-095A-6

Query Match 79.2%; Score 550.5; DB 19; Length 131;
Best Local Similarity 80.3%; Pred. No. 7e-47;
Matches 106; Conservative 8; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTOTPLSLPVSGDQVSIQSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFVIPASSDDVFMOTPLSLPVSLGDAQSISCRSSQSLVHSNGNTYLEW 59
QY 61 YLHKPGKSPQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYCLOGTHQP 120
DB 60 YLQKPGKSPKLLIYKYSNRFSGVDPDRFSGSGGTDTFLKISRVEAEDLGYYVCFQGSHPV 119
QY 121 YTFGGGKLEIK 132
DB 120 YTFGGGKLEIK 131

RESULT 9
US-08-134-346A-50
Sequence 50, Application US/08134346A
GENERAL INFORMATION:
APPLICANT: do Couto, F.J.R.
APPLICANT: Ceriani, R.L.C.
TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrager, Chong & Flaherty
STREET: 300 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10022-7499
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,346A
FILING DATE: 08-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Onofrio, Dara L.
REGISTRATION NUMBER: 34,889
REFERENCE/DOCKET NUMBER: CLT 149,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-826-6565
TELEFAX: 212-826-5909
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-134-346A-50

Query Match 77.3%; Score 537.5; DB 5; Length 131;
Best Local Similarity 77.3%; Pred. No. 1.4e-45;
Matches 102; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

APPLICANT: Herizawa, Nobufusa
 APPLICANT: Iakahara, Kaori
 APPLICANT: Chikawa, Kimihisa
 APPLICANT: Onohara, Shin
 TITLE OF INVENTION: ANTI-Fas RECOMBINANT ANTIBODIES AND DNA THEREFOR
 NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Frishauf, Holtz, Goodman, Langer & Chick,
 ADDRESSEE: P.C.
 STREET: 7/7 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10017-2023
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/827,223
 FILING DATE: 27-MAR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP Hei 8-78570
 FILING DATE: 01-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Goodman, Herbert
 REGISTRATION NUMBER: 17081
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-319-4900
 TELEFAX: 212-319-5101
 TELEX: 236268
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 238 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PS-08-827-223-10

[illegible]

RESULT 13
US-08-827-223-10
; Sequence 10, Application US/08827223A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Nalahara, Kaori
; APPLICANT: Iclikawa, Kimihisa
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: ANTI-Pas RECOMBINANT ANTIBODIES AND DNA THEREFOR
; FILE REFERENCE:: 970093/HG
; CURRENT APPLICATION NUMBER: US/08/827,223A
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: JP Hei 8-78570
; EARLIER FILING DATE: 1996-04-01

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; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 238
; TYPE: prt
; ORGANISM: Mus musculus
US-08-827223-10

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[illegible]

RESULT 14
US-09-046-351-10
US-09-046-351-10 Application US/09046351A
GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Taruyama, Hideyuki
APPLICANT: Takahashi, Tohru
APPLICANT: Nakahara, Kaori
APPLICANT: Yonehara, Shin
TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
FILE REFERENCE: 980125/HG
CURRENT APPLICATION NUMBER: US/09/046.351A
CURRENT FILING DATE: 1998-03-23
EARLIER APPLICATION NUMBER: JP HEI 9-67938
EARLIER FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 238
TYPE: PRT
ORGANISM: Mus musculus
US-09-046-351-10

[illegible]

RESULT 15
US-09-523-095A-10
; Sequence 10, Application US/09523095A
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: UNO, Shinsuke

APPLICANT: OH-EDA, Masayoshi
APPLICANT: KIKUCHI, Yasufumi
TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN EV
FILE REFERENCE: 065678/0102
CURRENT APPLICATION NUMBER: US/09/523,095A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: JP 11-63557
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 131
TYPE: PRT
ORGANISM: Mus sp.
US-09-523-095A-10

Query Match 76.3%; Score 530.5; DB 19; Length 131;
Best Local Similarity 78.0%; Pred. No. 6.7e-45;
Matches 103; Conservative 9; Mismatches 19; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDQVVTOTPLSLPVSGDQVVISCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFWIPGSSDQVVTOTPLSLPVSLGDAQASICRSSLVHNSNGKTYLHW 59
QY 61 YLHRPGSQPLLIIYGISNRFSGVDPDRFSGSGGTDFTLKISTIKRPEDLGMYCYCQGTHOP 120
Db 60 YLQKPGSPKLLIIYKVSNRFSGVDPDRFSGSGSVTDFTLMSRVEAEDLGVIYFCSQSTHVP 119
QY 121 YTFGGGTKLEIK 132
Db 120 YTFGGGTKLEIK 131

Search completed: April 13, 2001, 17:37:49
Job time: 166 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2001, 15:36:09 ; Search time 28.17 seconds
(without alignments)
90.019 Million cell updates/sec

Title: US-08-700-737-12
Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPTFGGKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558.5	80.4	131	3	US-08-589-939-7
2	552.5	79.5	149	2	US-08-752-844-2
3	552.5	79.5	149	2	US-08-591-196-2
4	546.5	78.6	238	4	US-08-182-545-4
5	543.5	78.2	131	1	US-08-053-171-5
6	543.5	78.2	131	1	US-08-053-171-9
7	537.5	77.3	131	1	US-08-129-930B-95
8	527.5	75.9	173	5	PCT-US91-02942-3
9	527.5	75.9	173	5	PCT-US91-02946-3
10	519.5	74.7	131	1	US-07-977-696C-11
11	519.5	74.7	131	1	US-08-129-930B-11
12	513	73.8	127	1	US-08-482-882-45
13	513	73.8	127	2	US-08-483-389-45
14	513	73.8	127	2	US-08-487-113D-45
15	513	73.8	127	2	US-08-473-503-45
16	513	73.8	127	2	US-08-483-932-45
17	513	73.8	127	2	US-08-720-420A-45
18	513	73.8	127	3	US-08-714-017-45
19	513	73.8	127	3	US-08-475-680-45
20	492	70.8	263	2	US-08-752-844-66
21	485	69.8	135	1	US-08-259-372A-12
22	485	69.8	135	1	US-08-468-671-12
23	483	69.5	125	1	US-08-331-398A-67
24	483	69.5	125	2	US-08-331-397B-67
25	483	69.5	125	2	US-08-759-804A-66
26	481	69.2	110	1	US-08-244-626-2
27	481	69.2	238	2	US-08-224-591-12

28 481 69.2 238 2 US-08-392-338A-21 Sequence 21, Appl
29 481 69.2 238 2 US-08-926-789-12 Sequence 12, Appl
30 481 69.2 238 3 US-09-166-750-21 Sequence 21, Appl
31 481 69.2 238 3 US-09-166-093-21 Sequence 21, Appl
32 481 69.2 238 3 US-09-172-019-21 Sequence 21, Appl
33 481 69.2 238 4 US-09-166-094-21 Sequence 21, Appl
34 481 69.2 239 5 PCT-US93-11138-12 Sequence 12, Appl
35 481 69.2 240 2 US-08-392-338A-11 Sequence 11, Appl
36 481 69.2 240 3 US-09-166-750-11 Sequence 11, Appl
37 481 69.2 240 3 US-09-166-093-11 Sequence 11, Appl
38 481 69.2 240 3 US-09-172-019-11 Sequence 11, Appl
39 481 69.2 240 4 US-09-166-094-11 Sequence 11, Appl
40 481 69.2 246 1 US-08-237-341-7 Sequence 11, Appl
41 481 69.2 250 2 US-08-392-338A-15 Sequence 15, Appl
42 481 69.2 250 3 US-09-166-750-15 Sequence 15, Appl
43 481 69.2 250 3 US-09-166-093-15 Sequence 15, Appl
44 481 69.2 250 3 US-09-172-019-15 Sequence 15, Appl
45 481 69.2 250 4 US-09-166-094-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-589-939-7
; Sequence 7, Application US/08589939
; Patent No. 6015662
; GENERAL INFORMATION:
; APPLICANT: Hackett, Jr., John R.
; APPLICANT: Hoff, Jane A.
; APPLICANT: Ostrow, David H.
; APPLICANT: Golden, Alan M.
; TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
; TITLE OF INVENTION: CONTROLS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,939
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5865.US.01
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-589-939-7

Query Match 80.4%; Score 558.5; DB 3; Length 131;
Best Local Similarity 81.1%; Pred. No. 3.4e-47;
Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVVTTPLSLPVSFGDQVSI SCRSSQSLAKSYGNTYLSW 60

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Db 1 MKLPVRLV-LMFVWIPASSDDVMTQTLPLSPVSGDQASISCRSSQSLVHSYNTYLSW 59
QY 61 YLHKPGQSPOLLIIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPDLGMVYCIQGTQHP 120
Db 60 YLQKPGQSPKLLIYKVNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
QY 121 YTFGGGTLEIK 132
Db 120 WTEGGGTLEIK 131

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RESULT 2
US-08-752-844-2
; Sequence 2, Application US/08752844
; Patent No. 5935121
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 705141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-2

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Query Match 79.5%; Score 552.5; DB 2; Length 149;
Best Local Similarity 79.5%; Pred. No. 1.5e-46;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLVFWIPVSGDQVVTQTLPLSPVSGDQVSISSCRSSQSLAKSYNTYLSW 60
Db 1 MKLPVRLV-LMFVWIPASSDDVMTQTLPLSLPVLGQASISCRSSQSIHNSGNTYLEW 59
QY 61 YLHKPGSPOLLIIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPDLGMVYCIQGTQHP 120
Db 60 YLQKPGSPNLLIYFVSNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSHVP 119
QY 121 YTFGGGTLEIK 132
Db 120 WTEGGGTLEIK 131

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RESULT 3
US-08-591-196-2
; Sequence 2, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-196-2

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Query Match 79.5%; Score 552.5; DB 2; Length 149;
Best Local Similarity 79.5%; Pred. No. 1.5e-46;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLVFWIPVSGDQVVTQTLPLSPVSGDQVSISSCRSSQSLAKSYNTYLSW 60
Db 1 MKLPVRLV-LMFVWIPASSDDVMTQTLPLSLPVLGQASISCRSSQSIHNSGNTYLEW 59
QY 61 YLHKPGSPOLLIIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPDLGMVYCIQGTQHP 120
Db 60 YLQKPGSPNLLIYFVSNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSHVP 119
QY 121 YTFGGGTLEIK 132
Db 120 WTEGGGTLEIK 131

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RESULT 4
US-09-192-545-4
; Sequence 4, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuoka, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 79979570
; CURRENT APPLICATION NUMBER: US/09/192,545

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Query Match	78.2%	Score 543.5;	DB 1;	Length 131;
Best Local Similarity	78.0%;	Pred. No. 9.6e-46;		
Matches 103; Conservative	11; Mismatches	17; Indels	1; Gaps	1;

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Query Match          78.2%; Score 543.5; DB 1; Length 131;
Best Local Similarity 78.0%; Pred. No. 9.6e+46;
Matches 103; Conservative 11; Mismatches 17; Indels 1; Gaps 1;
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QY	1	MKLPVRLVLVLLFWLPIGSSGDVVVTQTPLSLPVSGFDGVISICSRSSQSIAKSXGNITYLSW	60
Dd	1	: :	
		1 MKLPVRLLV - LMFWIPASSDVMLTPTPLSPVSLGDOASISCRSSQSIVHNSNGNTYLEW	59
QY	61	YLHKPQGSPQLLIYGISNRFSGVPDRFSGSGSGTDFTLTKISTIKPEDIGMYCLOGTHOP	120
Dd		: :	
		60 YLKQFGSQPKLLISKVSINRFSVDPDRFSGSGSGTDFTLKLISRVAEDLGYYTCFGSHWP	119
QY	121	YTFFGGTGLEIK	132
Dd		:	
		120 FTFFGSCTGLEIK	131
Dd		:	

RESULT 7
US-08-129-930B-95

RESULT 10
US-07-977-696C-11
Sequence 11, Application US/07977696C
Patent No. 5792852
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
TELEFAX: (510) 748-6688
TELEX: n.a.

```

RESULT 11
US-08-129-930B-11
; Sequence 11, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 NO. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-11

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US-08-482-882-45

Query Match 73.8%; Score 513; DB 1; Length 127;
Best Local Similarity 78.1%; Pred. No. 8.3e-43;
Matches 100; Conservative 9; Mismatches 17; Indels 2; Gaps 2;

Qy 6 RLLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKP 65
Db 1 RLLV-LMXWIPVSSDAVMTQTPLSLPVSLGDAQISCRSSQSLVHSDTYLHWYLOKP 59
Qy 66 GQSPOLLYIGVSNRFSGVDPDRF-SGSGSGTDTFTLKISTIKPEDLGMVYCLQGTHTQPTFG 124
Db 60 GQSPOLLYIKVSNRFSGVDPDRFSGSGSGTDTFTLKLSRVEADLGVYFCSTHTVPTFG 119
Qy 125 GGTGLEIK 132
Db 120 GGTGLEIK 127

RESULT 13

US-08-483-389-45

; Sequence 45, Application US/08483389
; Patent No. 5811517
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-RELATED PROTEIN
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; Zip: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Suh, Young J.
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/32760
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear

us-08-700-737-12.ra1

Query Match 74.7%; Score 519.5; DB 1; Length 131;
Best Local Similarity 77.3%; Pred. No. 2e-43;
Matches 102; Conservative 10; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSLGDAQISCRSSQSLVHSDTYLHWYLOKP 59
Qy 61 YLHKPQVQ:POLLYIGVSNRFSGVDPDRFSGSGTDTFTLKISTIKPEDLGMVYCLQGTHTQ 120
Db 60 FLQKSGQ:PKLLIYRASIRFSGVDPDRFSGSGTDTFTLKISRVEADLGVYFCFQGTHTP 119
Qy 121 YTFGGGTGLEIK 132
Db 120 WTFGGGTGLEIK 131

RESULT 12

US-08-482-882-45

; Sequence 45, Application US/08482882
; Patent No. 5773218
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6100 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; Zip: 60605

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5773218and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 26-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Sat Apr 14 08:10:17 2001

TELEFAX: (312) 474-0448
 TELEEX: 25-3856
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 177 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-473-503-45

Query Match 73.8%; Score 513; DB 2; Length 127;
 Best Local Similarity 78.1%; Pred. No. 8.3e-43;
 Matches 100; Conservative 9; Mismatches 17; Indels 2; Gaps 2;
 QY 6 RLIVLLWIPVSGDVVVTQTPLSLPVSGDQVSIICRSQSLSAKSYGNTVLSWYLHKP 65
 Db 1 RLLV-LM.WIPVSSDAVMTQTPLSLPVSLGDAQSICRSQSLVHNSGDTYLVHWYLOKP 59
 QY 66 GQSPQLLYGISNRFGVPDRF-SGSGSGTDFTLKISTIKPEDLGMYYCLOGTHOPYTFG 124
 Db 60 GQSPQLLYKVSNRFGVPDRFSGSGSGTDFTLKLSRVEADLGVYFCQSTHVPYTFG 119
 QY 125 GGTKEIK 132
 Db 120 GGTKEIK 127

Search completed: April 13, 2001, 15:36:11
 Job time: 129 sec

RESULT 2
MHMS18
Ig heavy chain precursor V region (B1-8) - mouse
N:Contains: Ig heavy chain precursor V region 186-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C:Accession: A90809; B90809; A22769; A02034; A02036
R:R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies:
A:Reference number: A90809; MUID:81234548
A:Accession: A90809
A:Molecule type: DNA
A:Residues: 1-139 <B18>
A:Cross-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
A:Accession: B90809

[illegible]

Matches 111; Conservative 4;

Query Match 76.1%; Score 576; DB 2; Length 131;
Best Local Similarity 82.8%; Pred. No. 4.7e-42;
Matches 111; Conservative 4; Mismatches 15; Indels

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:40:18 ; Search time 21.32 Seconds
(without alignments)
224.942 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757

Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGDYDAIDWGQTSVTYSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	599.5	79.2	139	1 HV07_MOUSE	P01751 mus musculus
2	559	73.8	138	1 HV48_MOUSE	P03980 mus musculus
3	556	73.4	117	1 HV06_MOUSE	P01750 mus musculus
4	554.5	73.2	117	1 HV11_MOUSE	P01755 mus musculus
5	543	71.7	117	1 HV03_MOUSE	P01749 mus musculus
6	537	70.9	117	1 HV09_MOUSE	P01753 mus musculus
7	532	70.3	140	1 HV02_MOUSE	P01746 mus musculus
8	527	69.6	117	1 HV04_MOUSE	P01748 mus musculus
9	525	69.4	117	1 HV09_MOUSE	P06328 mus musculus
10	519	68.6	117	1 HV10_MOUSE	P01754 mus musculus
11	497	65.7	136	1 HV15_MOUSE	P01759 mus musculus
12	479.5	63.3	120	1 HV50_MOUSE	P06329 mus musculus
13	468	61.8	120	1 HV03_MOUSE	P01747 mus musculus
14	447	59.0	117	1 HV12_MOUSE	P01756 mus musculus
15	447	59.0	121	1 HV01_MOUSE	P01745 mus musculus
16	445	58.9	117	1 HV52_MOUSE	P06327 mus musculus
17	445	58.8	117	1 HV13_MOUSE	P01757 mus musculus
18	444	58.7	117	1 HV14_MOUSE	P01758 mus musculus
19	441.5	58.3	118	1 HV51_MOUSE	P06330 mus musculus
20	422.5	55.8	147	1 HV16_MOUSE	P01744 homo sapien
21	412	54.4	117	1 HV1C_HUMAN	P23083 homo sapien
22	398	52.6	117	1 HV1B_HUMAN	P01743 homo sapien
23	348	46.0	117	1 HV42_MOUSE	P01812 mus musculus
24	347.5	45.9	114	1 HV00_MOUSE	P01741 mus musculus
25	341.5	45.1	119	1 HV38_MOUSE	P01808 mus musculus
26	341.5	45.1	136	1 HV16_MOUSE	DISULFID 41 115
27	339	44.8	142	1 HV01_RAT	P01783 mus musculus
28	335	44.3	117	1 HV41_MOUSE	P01805 rattus norv
29	333.5	44.1	119	1 HV37_MOUSE	P01811 mus musculus
30	331.5	43.8	146	1 HV21_HUMAN	P01807 mus musculus
31	327	43.2	118	1 HV39_MOUSE	P06331 homo sapien
32	325.5	43.0	119	1 HV40_MOUSE	P01809 mus musculus
33	319	42.1	121	1 HV3J_HUMAN	P01810 mus musculus
					P01771 homo sapien

34 316 41.7 125 1 HV1F_HUMAN P06326 homo sapien
35 312 41.2 117 1 HV1A_HUMAN P01742 homo sapien
36 311.5 41.1 122 1 HV3G_HUMAN P01768 homo sapien
37 308 40.7 115 1 HV32_MOUSE P01801 mus musculus
38 306.5 40.5 126 1 HV3K_HUMAN P01772 homo sapien
39 306 40.4 113 1 HV30_MOUSE P01799 mus musculus
40 305.5 40.4 120 1 HV1H_HUMAN P0421 homo sapien
41 304 40.2 116 1 HV36_MOUSE P01806 mus musculus
42 303.5 40.1 124 1 HV1D_HUMAN P01760 homo sapien
43 302.5 40.0 111 1 HV35_MOUSE P01804 mus musculus
44 301 39.8 113 1 HV27_MOUSE P01796 mus musculus
45 301 39.8 123 1 HV25_MOUSE P01794 mus musculus

ALIGNMENTS

RESULT 1
HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; J00529; AAA38170.1; -
CC PIR; A02034; MHMS18.
CC InterPro; IPR003006; -
CC Pfam; PF00047; ig; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC DOMAIN 20 49 FRAMEWORK 1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
CC DOMAIN 55 68 FRAMEWORK 2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
CC DOMAIN 86 117 FRAMEWORK 3.
CC DOMAIN 118 124 D SEGMENT.
CC DOMAIN 125 139 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 139
CC SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 79.2%; Score 599.5; DB 1; Length 139;
Best Local Similarity 80.7%; Pred. No. 2.4e-51;
Matches 113; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

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QY 1 MGWSCIILFLVSTATSVHSGVQLQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
DB 1 MGWSCIIMIPLAATATGATGSHVQVQLQPGAEVLKPGASVKLSCKRSGYTFSTSYNMHWKQRP 60
QY 61 GQGLEWICIDPESNTNYSQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
DB 61 GQGLEWICIDPESNTNYSQKFKSKATLTVDKPPSTAYMQLSSLTSEDSAVYYCARYD 120
QY 121 DGWDYAILYWGQGTSTVSS 140
DB 121 YGSSY-FIYWGQGTTLTVSS 139
RESULT 2
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8424078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR InterPro; IP003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;
Query Match 73.8%; Score 559; DB 1; Length 138;
Best Local Similarity 75.9%; Pred. No. 2e-47;
Matches 107; Conservative 12; Mismatches 18; Indels 4; Gaps 2;
QY 1 MGWSCIILFLVSTATSVHSGVQLQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
DB 1 MGWSCIIMIPLAATATGATGSHVQVQLQPGAEVLKPGASVKLSCKRSGYTFSTSYNMHWKQRP 60
QY 61 GQGLEWICIDPESNTNYSQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARG-G 119
DB 61 GQGLEWICIDPESNTNYSQKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARSDG 120
QY 120 YGWDYAILYWGQGTSTVSS 140
DB 121 YIDW---FVWGQGTTLTVSS 138
RESULT 3
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR; A02032; HVM502.
CC InterPro; IP003006; -.
CC Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
Query Match 73.4%; Score 556; DB 1; Length 117;
Best Local Similarity 89.7%; Pred. No. 3.2e-47;
Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 MGWSCIILFLVSTATSVHSGVQLQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
DB 1 MGWSCIIMIPLAATATGATGSHVQVQLQPGAEVLKPGASVKLSCKRSGYTFSTSYNMHWKQRP 60
QY 61 GQGLEWICIDPESNTNYSQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCA 116
DB 61 GQGLEWIGRIHPDSDTNYSQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116
RESULT 4
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
CC -----
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CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 FRAMEWORK 3.
FT DOMAIN 123 137 D SEGMENT.
FT DISULFID 41 115 JH2 SEGMENT.
FT NON_TER 137 137 BY SIMILARITY.
SQ SEQUENCE 137 AA; 15200 MW; ADD5861BF44B8EC9 CRC64;

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Query Match 73.2%; Score 554.5; DB 1; Length 137;
 Best Local Similarity 74.1%; Pred. No. 5.4e-47;
 Matches 106; Conservative 9; Mismatches 19; Indels 9; Gaps 2;

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QY 1 MCGWSCIILFLVSTATSVHSQVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMHVWVQRP 60
DB 1 MCGWSCIILFLVATATGVHSQVLOQPGAEVLKPGTSVKLSCKASGYTFTSYLMHVWVQRP 60
QY 61 GGLGEWIGEIDPSESTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCAR--- 117
DB 61 GGLGEWIGRIDNSGTTYNEHRSKATLTIDKPSSTAYMQLSSLTSDSAVYYCARYRL 120
QY 118 GCGDCWDYDAIDYWGOGTSVTSS 140
DB 121 GRY-----FDYWGOGTTLTVSS 137

```

```

RESULT 5
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC
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```

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CC EMBL; J00536; AAA38605.1; -.
CC PIR; A02031; HVMS3.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

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Query Match 71.7%; Score 543; DB 1; Length 117;
 Best Local Similarity 88.0%; Pred. No. 5.9e-46;
 Matches 103; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MCGWSCIILFLVSTATSVHSQVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMHVWVQRP 60
DB 1 MCGWSCIILFLVATATGVHSQVLOQPGAEVLKPGTSVKLSCKASGYTFTSYMDVWVQRP 60
QY 61 GGLGEWIGEIDPSESTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCAR 117
DB 61 GGLGEWIGNIYPSDSETHYNOKFKDKATLTVDKSSSTAYMQLSSLTSDSAVYYCAR 117

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RESULT 6
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC
CC PIR; B02034; HVMS61.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

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Query Match 70.9%; Score 537; DB 1; Length 117;
 Best Local Similarity 84.6%; Pred. No. 2.2e-45;
 Matches 99; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

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21-JUL-1986 (Rel. 01, Last sequence update)
13-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bellmore D.;
RT "heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SPT OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02030; HWS23.
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 69.6%; Score 527; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 2.le-44;
Matches 98; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVLTATSVHVSQVLOQPGAEILVKPGTSVKLCKGCGYGTFTSYMMHWKORP 60
1 MGWSCIIILFLVAANGVHVSQVLOQPGTGLVKPGASVKLCKASGYGTFTSYMMHWKORP 60

DB 1 MGWSCIIILFLVLTATSVHVSQVLOQPGAEILVKPGTSVKLCKGCGYGTFTSYMMHWKORP 117
1 MGWSCIIILFLVAANGVHVSQVLOQPGTGLVKPGASVKLCKASGYGTFTSYMMHWKORP 117

QY 61 GQGLEWIGEIDPSSENTNMYNKFKGKATFLVDISSTAYMOLSSLTSDSAVYYCAR 117
1 GQGLEWIGINPGNGGTYNEKFKSKVTLTVDKSSSTAYTQLSSLTSDSAVYYCAR 117

DB 61 GQGLEWIGINPGNGGTYNEKFKSKVTLTVDKSSSTAYTQLSSLTSDSAVYYCAR 117
1 GQGLEWIGINPGNGGTYNEKFKSKVTLTVDKSSSTAYTQLSSLTSDSAVYYCAR 117

RESULT 9
HV49_MOUSE STANDARD; PRT; 117 AA.
ID HV49_MOUSE
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC Cell 40:271-281(1985)).

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CC EMBL; M13788; AAA38506.1;
DR PIR; A02035; HWSB4;
DR InterPro; IPR003006;
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 69.4%; Score 525; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 3.2e-44;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
DB 1 MGWSCIMFLAATATGVSHPVLOQPGAEVLKPGASVKLSCKASGYTFTSYMMHWKQRP 60
QY 61 GCGLEWIGIDPSESTNTYNOKEFKGKATLTVDISSTAYMOLSSLTSEDSAVYYCAR 117
DB 61 GRGLEWIGNIDPNSGTYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCTR 117

RESULT 10
HV10_MOUSE
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 145 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
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CC -----
CC EMBL; J00533; AAA38602.1;
DR PIR; C02034; HWSB45.
DR InterPro; IPR003006;
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

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FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 68.6%; Score 519; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 1.2e-43;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
DB 1 MGWSCIMFLAATATGVSHPVLOQPGAEVLKPGASVKLSCKASGYTFTSYMMHWKQRP 60
QY 61 GCGLEWIGIDPSESTNTYNOKEFKGKATLTVDISSTAYMOLSSLTSEDSAVYYCAR 117
DB 61 GRGLEWIGNIDPNSGTYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR 117

RESULT 11
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -----
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CC -----
CC EMBL; J00494; AAA38130.1;
DR PIR; A02042; HWSB1.
DR InterPro; IPR003006;
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 65.7%; Score 497; DB 1; Length 136;
Best Local Similarity 68.3%; Pred. No. 2e-41;
Matches 97; Conservative 12; Mismatches 25; Indels 8; Gaps 2;

QY 1 MGWSCILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
DB 1 MGWSCIMFLAATATGVSHPVLOQPGAEVLKPGASVKLSCKGKGYTFTSYMMHWKQSH 60
QY 61 GCGLEWIGIDPSESTNTYNOKEFKGKATLTVDISSTAYMOLSSLTSEDSAVYYCAR--G 118
DB 61 AKSLEWIGISTYNGTSTYNOKEFKGKATMTVDKSSSTVHMLARLTSEDSANLYCARYTG 120

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QY 119 GYDGDYDAIDYWGQTSVTSS 140
DB 121 NY-----FDYWGQGTTLTVSS 136

RESULT 12
HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=1090;
RN [1]
RP SEQUENCE.
RA MEDLINE=8418;519; PubMed=6201362;
RX Dildrop R., Hovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region (determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:511-523(1984).
DR PIR: A02037; MHMS15.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 120 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
FT SEQUENCE 130 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 63.3%; Score 479.5; DB 1; Length 120;
Best Local Similarity 75.2%; Pred. No. 8.4e-40;
Matches 91; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 20 QVLOQP:AEVLVPGTSVKLSCKGYGTYFTSYMMHWKORPGGLEWIGIDPSESNTNY 79
DB 1 QVLOQP:ETLVKPGASVNLSCASGYTFTSYMMHWIRQPGGLEWIGINPNSGNTNY 60
QY 80 NORFKGKATLTVDISSSTAYMQLSLTSDSAVYICARGYDGDYDAIDYWGQTSVTSS 139
DB 61 NEFKSKATLTVDKSSATYMQLSLTSDSAVYICARWDYEG-DRYFDVWGTTTSTS 119
QY 140 S 140
DB 120 S 120

RESULT 13
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FRGM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RX Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).

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CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR: A02028; HYMSG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF04B4A167B654AF CRC64;

Query Match 61.8%; Score 468; DB 1; Length 120;
Best Local Similarity 74.2%; Pred. No. 1.1e-38;
Matches 89; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 21 VLOQP:GAELVPGTSVKLSCKGYGTYFTSYMMHWKORPGGLEWIGIDPSESNTNY 80
DB 1 VLOQSGAELVRAGSVKMSCKASGYTFTSYGNWKORPGGLEWIGINPGNYTKYN 60
QY 81 QKFKGKATLTVDISSSTAYMQLSLTSDSAVYICARGYDGDYDAIDYWGQTSVTSS 140
DB 61 EKFCKGKATLTVDKSSSTAYMQLSLTSDSAVYICARSVYIGSYFYDYGQGTTLTVSS 120

RESULT 14
HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RX Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MHMS4E.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 59.0%; Score 447; DB 1; Length 117;
Best Local Similarity 71.1%; Pred. No. 1.1e-36;
Matches 86; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 20 QVLOQP:GAELVPGTSVKLSCKGYGTYFTSYMMHWKORPGGLEWIGIDPSESNTNY 79
DB 1 EVLOQSGPGLVLPFGASVKMSCKASGYTFTSYMMHWKQSHGSKSLEWIGIDPNSNGTST 60
QY 80 NORFKGKATLTVDISSSTAYMQLSLTSDSAVYICARGYDGDYDAIDYWGQTSVTSS 139
DB 61 NORFKGKATLTVDKSSSTAYMQLSLTSDSAVYICAR-----DYDWYFDVWGAGTTTSTS 116
QY 140 S 140
DB 117 S 117

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RESULT 15
HV01_MOUSE
ID HV01_MOUSE STANDARD: PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RL region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11
DR InterPro; IPR003006;
DR Pfam; PF00047; 19; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
```

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Query Match 59.08; Score 447; DB 1; Length 121;
Best Local Similarity 69.4%; Pred. No. 1.2e-36;
Matches 84; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

Qy 20 QVQLQQPGAEVLKPKTSVKLSCKGYGTFTSYWMHWKQRPQGLEWIGTIDPSESNTNY 79
: |||| |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 1 EAQLQSGAEVLKPKTSVKLSCKAGYFTNWIWGWKRPQGLEWIGDIYPCGGFTNY 60

Qy 80 NQKFKGKATLVDTSSSTAYNQLSLSLTSSEDSAVYICARGGYDWDYDAIDYWGQGTSTVTS 139
: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 61 NDNLKGRATLTADTSSSTAYIQLSLSLTSSEDSAVYICARGIYNSSPYFDSWGQGTTLTVS 120

Qy 140 S 140
Db 121 S 121
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Search completed: April 13, 2001, 15:40:19
Job time: 272 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:39:54 ; Search time 56.51 Seconds
(without alignments)
290.375 Million cell updates/sec

Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIIFLVSTATSVHSQ.....DGWDYATDYWGQGSVTYSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Model	Number of hits	Number of parameters
Model 1	374700	374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : SPTREMBL_15:★

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1: sp_archaea:*
2: sp_bacteria:*
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3: sp_fungi: *
4: sp_human: *
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5: sp_invertebrate:*

6: sp_maint: *
7: sp_mhc: *

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8: sp_organelle:*
9: sp_phage:*
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10: sp_plant:*
11: sp_rodent.*
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12: sp_unclassified:
13: 
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14: sp_virus:*
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ter than or equal to the value obtained by analysis of the

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Match	Length	DB	ID
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62.5	117	11	0908
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61.4	110	11	Q9JH
61.1	114	11	Q9JH

60.6	117	11	Q9QX
60.6	118	11	Q9QY
60.6	119	11	Q9QZ

110	11	Q9JL
58.5	11	Q9JL

57.7	117	11	Q9Z1
54.8	124	4	Q9UL9

54.7	119	4	Q9UL9
54.5	110	11	Q9JH

	Q9Y29	4	150	53.4
	CONC	4	125	51.5

51.0	109	11	Q9JL
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51.0	137	4	Q9597
47.1	116	4	Q9UL8

	Q9QY	Q9UL
46.8	298	11
42.7	116	4

41.9	113	4	Q9UL9
41.4	147	4	Q9VE0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	%		Length	DB	ID	Description
		Score	Match				
1	473	62.5	117	11	Q9XE9	Q9xe9 mus musculu	
2	464.5	61.4	110	11	Q9JL77	Q9jl77 mus musculu	
3	462.5	61.1	114	11	Q9JL81	Q9jl81 mus musculu	
4	459	60.6	117	11	Q9XF0	Q9xf0 mus musculu	
5	458.5	60.6	118	11	Q9Z1C4	Q9z1c4 mus musculu	
6	442.5	58.5	109	11	Q9JL75	Q9jl75 mus musculu	
7	437	57.7	117	11	Q9Z1C6	Q9z1c6 mus musculu	
8	414.5	54.8	124	4	Q9JL92	Q9jl92 homo sapien	
9	414	54.7	119	4	Q9JL94	Q9jl94 homo sapien	
10	412.5	54.5	110	11	Q9JL83	Q9jl83 mus musculu	
11	404	53.4	150	4	Q9Y298	Q9y298 homo sapien	
12	390	51.5	125	4	Q9Y298	Q9y298 homo sapien	
13	386	51.0	109	11	Q9JL85	Q9jl85 mus musculu	
14	386	51.0	157	4	Q9S978	Q9s978 homo sapien	
15	356.5	47.1	116	4	Q9JL89	Q9jl89 homo sapien	
16	354.5	46.8	298	11	Q9YF0	Q9yf0 mus musculu	
17	323	42.7	116	4	Q9JL93	Q9jl93 homo sapien	
18	317	41.9	113	4	Q9JL90	Q9jl90 homo sapien	
19	313.5	41.4	147	4	Q9Y509	Q9y509 homo sapien	

20	301.5	39.8	118	4	Q9UL91	homo sapien
21	301	39.8	131	4	Q9UL88	homo sapien
22	300	39.6	121	4	Q9UL71	homo sapien
23	294.5	38.9	122	4	Q9UL84	homo sapien
24	291	38.4	119	4	Q9UL73	homo sapien
25	284.5	37.6	118	4	Q9UL72	homo sapien
26	284.5	37.6	150	4	Q9S973	homo sapien
27	278.5	36.8	437	11	Q9RLA4	mus musculus
28	278	36.4	102	11	Q9JL79	mus musculus
29	275.5	36.4	124	6	Q9N0W6	cryptotlagus
30	273.5	36.1	124	6	Q9N0W4	cryptotlagus
31	265	35.0	95	4	Q9ULB6	homo sapien
32	253	33.4	112	4	Q9UGP3	homo sapien
33	252	33.3	104	4	Q9UL87	homo sapien
34	239.5	31.6	122	4	Q9UL75	homo sapien
35	216	28.5	121	4	Q9UL96	homo sapien
36	212	28.0	82	4	Q75729	homo sapien
37	203	26.8	88	4	Q75737	homo sapien
38	202	26.7	76	4	Q75742	homo sapien
39	199	26.3	118	4	Q9UL74	homo sapien
40	196	25.9	77	4	Q75741	homo sapien
41	193.5	25.6	416	4	Q9NP66	homo sapien
42	188.5	24.9	77	4	Q75726	homo sapien
43	188.5	24.9	81	4	Q75719	homo sapien
44	187.5	24.8	78	4	Q75730	homo sapien
45	187	24.7	77	4	Q75728	homo sapien

ALIGNMENTS

[illegible]

Query Match	62.5%;	Score 473;	DB 11;	Length 117;
Best Local Similarity	75.2%;	Pred. No. 3.2e-41;		
Matches 91;	Conservative 10;	Mismatches 16;	Indels 4;	Gaps 1;
QY	20	QVQLQQPQGAELVKPQTSVKLSCKGKGYGTYFTSYNMHWVKQRPQGCGLEWIGETDPSESNTNY	79	
Db	1	EVQLQSGPELVKPGASVKMCKRACGYTFDDYMKWKVKQSHGSKSLEWIGDINPNNGCTSY	60	
QY	80	NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGCYDGDWDYDAIDYWGQGTSTVTVS	139	
Db	61	NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY----	YAMDYWGQGTSTVTVS	116
QY	140	S 140		
Db	117	S 117		
RESULT	2			

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Q9JL77
ID Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77 TREMBLrel. 15, Created)
DT 01-OCT-2000 TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206029; AAF69327.1; -.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 61.4%; Score 464.5; DB 11; Length 110;
Best Local Similarity 79.3%; Pred. No. 2.2e-40;
Matches 88; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 30 LVKPGTSVKLSCKGYGTYFTSYMMHWKQKPGQGLEWIGEIDPSESNTNMQKFKGKATL 89
DB 3 LVKPGASVKLSCKASGYTFTSYMMHWAKQKPGQGLEWIGEIDPSEHTNNEKFKGKATL 62
QY 90 TVDTSSTAYMQLSSLTSEDSAVYICARGYDGDWDYDAIDYWGQTSVTSS 140
DB 63 TVDTSSTAYVDLSLTSEDSAVYICAR---QRRNYAMDYWGQTSVTSS 110

RESULT 3
ID Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206025; AAF69323.1; -.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12829 MW; 404895FDE6BA56F8 CRC64;

Query Match 61.1%; Score 462.5; DB 11; Length 114;
Best Local Similarity 77.9%; Pred. No. 3.7e-40;
Matches 88; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 29 ELVKPGTSVKLSCKGYGTYFTSYMMHWKQKPGQGLEWIGEIDPSESNTNMQKFKGKAT 88
DB 2 QLVKPGASVKISCKASGYSTFTSYMMHWKQKPGQGLEWIGMDPDSSETRLNQKFKKAT 61
QY 89 LTVDTSSTAYMQLSSLTSEDSAVYICARGYDGDWD-VAIDYWGQTSVTSS 140
DB 62 LTVDKSSTAYMQLSSPTESDSAVYICARSNYGSGLYFDYWGQGTTLTVSS 114
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RESULT 4
Q9QXF0 PRELIMINARY; PRT; 117 AA.
ID Q9QXF0
AC Q9QXF0
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 60.6%; Score 459; DB 11; Length 117;
Best Local Similarity 72.7%; Pred. No. 8.7e-40;
Matches 88; Conservative 11; Mismatches 18; Indels 4; Gaps 1;

QY 20 OVQLOQPGAEIVKPGTSVKLSCKGYGTYFTSYMMHWKQKPGQGLEWIGEIDPSESNTNY 79
DB 1 EVQLOQSGPELVKPGASVKMSCKASGYTFTDYMMKWKSHGKSLWIGDINPNCGTSY 60
QY 80 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARGYDGDWDYDAIDYWGQTSVTSS 139
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYICARDK---DYFDYWGQGTTLTVS 116
QY 140 S 140
DB 117 S 117

RESULT 5
Q9Z1C4 PRELIMINARY; PRT; 118 AA.
ID Q9Z1C4
AC Q9Z1C4
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matlis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 60.6%; Score 458.5; DB 11; Length 118;
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Best Local Similarity 71.8%; Pred. No. 9.8e-40;
Matches 89; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

QY 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTNY 79
DB 1 QVQVQSGAEALPWAASVKLSCKASGYFTSYMMHWKQRPQGLEWIGAIYPGDGTSY 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSSLTSED$AVYICAR--GGYDGDWDYDAIDYWGQGTSTV 136
DB 61 TQKFGKATLTADKSSSTAYMQLSSLTSED$AVYICARTVGGY-----FDYWGQGTTL 114
QY 137 TVSS 140
DB 115 TVSS 118

RESULT 6
Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206031; AAF69329.1; -.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12118 MW; FT65E441BBF936A6 CRC64;

Query Match 58.5%; Score 442.5; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 3.9e-38;
Matches 86; Conservative 8; Mismatches 14; Indels 5; Gaps 2;

QY 29 ELVKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTNYNQKFKGKAT 88
DB 1 ELVKPGASVKMSCKASGYFTSYMMHWKQRPQGLEWIGYINPYNDGTYKNEKEKGRAT 60
QY 89 LTVDISSTAYMQLSSLTSED$AVYICAR--GGYDGDWDYDAIDYWGQGTSTVSS 140
DB 61 LTSDKSSSTAYMQLSSLTSED$AVYICARDGNYRGF----DYWGQGTTLTVSS 109

RESULT 7
Q9Z1C6 PRELIMINARY; PRT; 117 AA.
AC Q9Z1C6;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
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endothelial cells.";
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78799; AAD00291.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig: 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match 57.7%; Score 437; DB 11; Length 117;
Best Local Similarity 70.2%; Pred. No. 1.6e-37;
Matches 85; Conservative 8; Mismatches 24; Indels 4; Gaps 2;

QY 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTNY 79
DB 1 QVLOQSGPQLVRPGTSVKISCKASGYFTSYMMHWKQRPQDLEWIGMIDPSDSEVL 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSSLTSED$AVYICARGYDGDWDYDAIDYWGQGTSTVTS 139
DB 61 NORLKDKAILTVDKSSNTAYMQFSGPTSED$AVYICTRGEV-SW---PAYWGQGTTLTVTS 116
QY 140 S 140
DB 117 A 117

RESULT 8
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig: 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 54.8%; Score 414.5; DB 4; Length 124;
Best Local Similarity 64.5%; Pred. No. 3.4e-35;
Matches 80; Conservative 17; Mismatches 24; Indels 3; Gaps 1;

QY 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTNY 79
DB 1 EVQLVESCAEVKKPCASVKVSKASGYFTSSYYMMHWKQRPQGLEWGMGIIINPSGGSTSY 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSSLTSED$AVYICARGYDGDWDY---IDYWGQGTSTV 136
DB 61 AQKQGRVTMTDRTSTSTVYMELSLRSED$AVYICARGLYVVVPAAFSRFDYWGQGTTLV 120
QY 137 TVSS 140
DB 121 TVSS 124

RESULT 9
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035019; AAD56255.1; -
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; ig: 1.
FT NON_TER 1
FT SEQUENCE 125 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 51.5%; Score 390; DB 4; Length 125;
Best Local Similarity 60.0%; Pred. No. 1.1e-32;
Matches 75; Conservative 16; Mismatches 30; Indels 4; Gaps 1;
QY 20 QVQLQPGAEVLVPGTSVKLSCKGYGTFYSYHWHVWVQKRPQGGLEWIGIDPSESNTNY 79
DB 1 EQLVSEGAELVKRPGASVKYKSCASGYTFGTGYHWHVWVQKRPQGGLEWIGIDPSESNTNY 60
QY 80 NQKFKGKATLVDISSTAYMQLSSLTSEDSAVYCYCAR----GGYDGDWDYADYWGQGT 135
DB 61 AQVQGRVMTWTRTTISTAYMELSLRLSDDTAVYCARSGGGRIAAAGDAFDWGGTM 120
QY 136 VTVSS 140
DB 121 VTVSS 125

RESULT 13
Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206021; AAF69319.1; -
DR NON_TER 1
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 51.0%; Score 386; DB 11; Length 109;
Best Local Similarity 64.6%; Pred. No. 2.5e-32;
Matches 73; Conservative 13; Mismatches 23; Indels 4; Gaps 1;
QY 28 AELVKPCTSVKLSCKGYGTFYSYHWHVWVQKRPQGGLEWIGIDPSESNTNYNPKFKGKA 87
DB 1 AELVKPGASVKLSCTASGNIETDTHYHWHVWVQKRPQGGLEWIGIDPAGTGHKSDPKFGKA 60
QY 88 TLTVDISSTAYMQLSSLTSEDSAVYCYARGYDGDWDYADYWGQGTSTVTVSS 140
DB 61 TITSDTSNTAYLQLSSLTSEDSAVYCYVRG-----AVVDYWGQGTALTIVSS 109

RESULT 14
O95978 PRELIMINARY; PRT; 157 AA.
AC O95978;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE VH1 PROTEIN PRECURSOR (FRAGMENT).
GN VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
patient with mixed cellularly Hodgkin's disease is associated with
somatic mutations within the untruncated regions of rearranged and
RT class switch recombinated Ig genes."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ005570; CAA06599.1; -
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; ig: 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT NON_TER 157 157
FT SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;

Query Match 51.0%; Score 386; DB 4; Length 157;
Best Local Similarity 51.4%; Pred. No. 3.9e-32;
Matches 75; Conservative 24; Mismatches 35; Indels 12; Gaps 2;
QY 1 MGSICILFLVSTATSVHVSQVQLQPGAEVLVPGTSVKLSCKGYGTFYSYHWHVWVQKRP 60
DB 1 MDWTWRVFCLLAVAPGVHVSQVQLVQSGAEIKRPGASVKVHCKTSGYVFTSYIHWVQRP 60
QY 61 GQGLEWIGIDPSESNTNYNPKFKGKATLVDISSTAYMQLSSLTSEDSAVYCYARGG- 119
DB 61 GQGLEWVGIGPGVGSTMAEKFQGLTMTNTSTTTVMYELSLRLREFDTAVYFCGRGR 120
QY 120 -----VDGDYADYWGQGTSTVTVSS 140
DB 121 WRSNGNYG-----HMQGGTPVTVSS 140

RESULT 15
Q9JL89 PRELIMINARY; PRT; 116 AA.
AC Q9JL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035025; AAD56261.1; -
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; ig: 1.
FT NON_TER 1
FT NON_TER 116 116
FT SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 47.1%; Score 356.5; DB 4; Length 116;
Best Local Similarity 60.3%; Pred. No. 2.8e-29;
Matches 70; Conservative 16; Mismatches 29; Indels 1; Gaps 1;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2001, 15:35:39 ; Search time 57.59 Seconds
(without alignments)
138.963 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757

Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGWDYALDYWGQTSVTYSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0401.*

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1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.*
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9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT.*
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12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	757	100.0	140	19 W53815	Murine Act-1 heavy
2	730	96.4	137	19 W53818	Protein sequence O
3	713	94.2	144	19 W53816	Consensus protein
4	632	83.5	180	19 W53813	Heavy chain of a h
5	615	81.2	464	19 W83041	Anti-Fas MAB HFE7A
6	615	81.2	464	21 B14747	Mouse anti-Fas ant
7	615	81.2	464	21 W90897	Murine anti-Fas an
8	597	78.9	464	16 R76088	MAB 55.1 heavy cha
9	594.5	78.5	443	18 W24025	Single chain antig
10	589	77.8	140	13 R27049	VH425 antibody clo
11	586	77.4	136	8 P70624	Sequence encoded b

12	586	77.4	136	18 W10584	Anti-hepatitis B h
13	586	77.4	136	18 W16340	Mouse-human chimae
14	586	77.4	136	18 W10239	Chimeric anti-hepa
15	586	77.4	136	19 W47510	Human anti-hepatit
16	586	77.4	136	19 W41054	Human anti-hepatit
17	586	77.4	136	19 W47517	Human anti-hepatit
18	586	77.4	136	20 W89535	Chimeric anti-hepa
19	583	77.0	143	16 R84554	MAB SCH94.03 heavy
20	567	74.9	470	21 W90933	Humanised anti-Fas
21	565	74.6	470	21 W90934	Humanised anti-Fas
22	564	74.5	470	19 W83037	Anti-Fas humanised
23	564	74.5	470	21 B14779	Humanised anti-Fas
24	564	74.5	470	21 W90929	Humanised HFE7A de
25	564	74.5	470	21 W90935	Humanised anti-Fas
26	556	73.4	145	19 W83038	Anti-Fas humanised
27	556	73.4	145	21 B14775	Fragment of humani
28	556	73.4	145	21 W90925	Humanised anti-Fas
29	556	73.4	470	19 W83036	Anti-Fas humanised
30	556	73.4	470	21 B14776	Humanised anti-Fas
31	556	73.4	470	21 W90926	Humanised HFE7A de
32	551.5	72.9	143	12 R12233	Mouse MAB 2E12 H c
33	551.5	72.9	144	12 R12355	Heavy chain variab
34	549	72.5	138	19 W50218	Amino acid sequenc
35	549	72.5	470	21 B08026	A dimeric anti-CD2
36	548.5	72.5	137	19 W44177	Monoclonal antibod
37	545	72.0	140	15 R55215	Murine variable re
38	545	72.0	470	21 W90936	Humanised HFE7A de
39	544.5	71.9	139	13 R29009	p64-h2 protein pro
40	543	71.7	140	18 W06213	MAB Co-1 heavy cha
41	543	71.7	140	20 W85061	Mouse Co-1 heavy c
42	538	71.1	119	18 W07436	Anti-DNA antibody
43	537	70.9	140	11 R09425	Co-1 Heavy Chain v
44	536.5	70.9	465	16 R66758	Anti-tobacco mosai
45	536	70.8	119	16 R79863	Anti-EGFR antibody

ALIGNMENTS

RESULT 1
ID W53815 standard; Protein; 140 AA.
XX AC W53815;

XX 14-JUL-1998 (first entry)

XX Murine Act-1 heavy chain variable region.

XX Mouse: Act-1 antibody; human alpha4-beta7 integrin;

XX Muscosal adressin cell adhesion molecule-1; MadCAM-1;

XX humanised antibody; murine antigen binding region; inhibition;

XX leukocyte infiltration of tissue; treatment; inflammatory disease;

XX inflammatory bowel disease.

XX Mus. sp.

Key	Location/Qualifiers
Peptide	1..19
Protein	/note= "signal peptide"
Protein	20..140
Protein	/note= "mature protein"

XX W09806248-A2.

XX 19-FEB-1998.

XX 06-AUG-1997; 97WO-0513884.

XX 15-AUG-1996; 96US-0700737.

XX (LEUK-) LEUKOSITE INC.

XX

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PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
XX Saldanha J;
DR WPI: 1998-159172/14.
XX N-PSDB; V2008.
XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
XX Example 1; Fig 2; 145pp; English.
PS Claim 27; Fig 9; 145pp; English.
XX The present sequence represents the heavy chain variable region of
CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
CC integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a
CC ligand of this particular integrin. The Act-1 antibody interferes with
CC alpha4-beta7 integrin binding to MadCAM-1, which is present of high
CC endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used
CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
CC leukocyte infiltration of tissues, e.g. for treating inflammatory
CC diseases such as inflammatory bowel disease. The immunoglobulin can
CC also be used for detection, isolation and diagnosis.
XX Sequence 140 AA;
SQ
Query Match 100.0%; Score 757; DB 19; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGWSCIIILVSTATSVHSGVQLQPGAEIVKPGTSVKLSCKGYGTYFTSYNMHWVKQRP 60
DB 1 mgwsciiilvstatsvhsqvlqpgaelvkpgtsvklsckgygtyftsymbhwvkqrp 60
QY 61 GQGLEWIEIDPSESNTNMQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
DB 61 gqglewieidpseantnynqkfkgtatltvdissstaymqllsstsedsavyyccargy 120
QY 121 DGWDYALDYWGQTSVTSS 140
DB 121 dgwdyaldywggtsvtss 140
RESULT 2
W53818
ID W53818 standard; Protein; 137 AA.
XX W53818;
XX W53818;
XX 14-JUL-1998 (first entry)
XX Protein sequence of murine variable heavy chain region of clone H2B#34.
XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease.
XX Mus sp.
XX WO9806248-A2.
XX 19-FEB-1998.
XX 06-AUG-1997; 97WO-US138B4.
XX 15-AUG-1996; 96US-0700737.
XX (LEUK-) LEUKOSITE INC.
XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
PI
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PI Saldanha J;
XX WPI: 1998-159172/14.
XX N-PSDB; V20089.
XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
XX Example 1; Fig 2; 145pp; English.
PS The present sequence represents the amino acid sequence comprising the
XX variable region of murine Act-1 antibody determined from clone H2B#34.
CC Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin
CC cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular
CC integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
CC to MadCAM-1, which is present of high endothelial venules in mucosal
CC lymph nodes. The present sequence was used to construct chimeric,
CC humanised Act-1 antibodies, which contain murine antigen binding regions.
CC The humanised immunoglobulin can be used to inhibit the interaction of
CC cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7.
CC It can be used for inhibiting leukocyte infiltration of tissues, e.g. for
CC treating inflammatory diseases such as inflammatory bowel disease. The
CC immunoglobulin can also be used for detection, isolation and diagnosis.
XX Sequence 137 AA;
SQ
Query Match 96.4%; Score 730; DB 19; Length 137;
Best Local Similarity 98.5%; Pred. No. 3.9e-53;
Matches 135; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWSCIIILVSTATSVHSGVQLQPGAEIVKPGTSVKLSCKGYGTYFTSYNMHWVKQRP 60
DB 1 mgwsciiilvstatsvhsqvlqpgaelvkpgtsvklsckgygtyftsymbhwvkqrp 60
QY 61 GQGLEWIEIDPSESNTNMQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
DB 61 gqglewieidpseantnynqkfkgtatltvdissstaymqllsstsedsavyyccargy 120
QY 121 DGWDYALDYWGQTSVT 137
DB 121 dgwdyaldywggtsvt 137
RESULT 3
W53816
ID W53816 standard; Protein; 144 AA.
XX W53816;
XX W53816;
XX 14-JUL-1998 (first entry)
XX Consensus protein sequence of the murine variable heavy chain region.
XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease.
XX Mus sp.
XX Key Location/Qualifiers
FH Misc-difference 2 /note= "not specified, encoded by RRA"
FT Misc-difference 3 /note= "not specified, encoded by TGS"
FT Misc-difference 4 /note= "not specified, encoded by ASC"
FT Misc-difference 5 /note= "not specified, encoded by TRK"
FT Misc-difference 6
```

FT Misc-difference 7 /note= "not specified, encoded by RTC"
 FT /note= "encoded by ATY"
 FT Misc-difference 8 /note= "not specified, encoded by YTC"
 FT Peptide 1..19 /note= "signal peptide"
 FT Protein 20..144 /note= "mature protein"
 FT Region 20..49 /note= "framework region 1"
 FT Region 50..54 /note= "CDR1"
 FT Region 55..68 /note= "framework region 2"
 FT Region 69..85 /note= "CDR2"
 FT Region 86..117 /note= "framework region 3"
 FT Region 118..130 /note= "CDR3"
 FT Region 131..141 /note= "framework region 4"
 FT
 PN WO9806248-A2.
 XX 19-FEB-1998.
 XX 06-AUG-1997; 97WO-US13884.
 XX 15-AUG-1996; 96US-0700737.
 XX (LEUK-) LEUKOSITE INC.
 XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX WPI; 1998-159172/14.
 DR N-PSDB; V20085.
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX Example 1; Fig 1; 145pp; English.
 XX The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse heavy chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 XX Sequence 144 AA;
 Query Match 94.2%; Score 713; DB 19; Length 144;
 Best Local Similarity 99.3%; Pred. No. 1e-51;
 Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 ILFLVSTATSVHSGVQLQPGAEIVKPGCSVKLSCKGYGYTFTSYMMHWVKRPGGLEW 66

Db 7 ILFLVSTATSVHSGVQLQPGAEIVKPGCSVKLSCKGYGYTFTSYMMHWVKRPGGLEW 66
 QY 67 IGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGYDGMWYA 126
 Db 67 Igeidpsesntnyngkfkgkatltcvdisstaymqsltsedseavyycarggydgwdya 126
 QY 127 IDYWGQGTSTVTVSS 140
 Db 127 idywgqgtstvtvss 140
 RESULT 4
 W53813
 ID W53813 standard; Protein; 180 AA.
 XX W53813;
 XX 14-JUL-1998 (first entry)
 XX Heavy chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; Inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 XX Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19 /note= "signal peptide"
 FT Protein 20..180 /note= "mature protein"
 FT
 XX WO9806248-A2.
 XX 19-FEB-1998.
 XX 06-AUG-1997; 97WO-US13884.
 XX 15-AUG-1996; 96US-0700737.
 XX (LEUK-) LEUKOSITE INC.
 XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX WPI; 1998-159172/14.
 DR N-PSDB; V20076.
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX Claim 20; Fig 11; 145pp; English.
 XX The present sequence represents the heavy chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 XX Sequence 180 AA;

Query Match 83.5%; Score 632; DB 19; Length 180;
 Best Local Similarity 85.9%; Pred. No. 5.8e-45;
 Matches 116; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 6 IILFLVSTSVHVSQVQLQPGAEVLKPGTSTVKLSCKGSGYFTFTSYMMHWKQRPQGGLE 65
 DB 6 VILFLVSTSVHVSQVQLQPGAEVLKPGTSTVKLSCKGSGYFTFTSYMMHWKQRPQGGLE 65

QY 66 WIGEIDP:ESNTNYNQKFKGATFLVDISSSTAYMOLSLTSEDSAVYYCARGGIDGWY 125
 DB 66 WIGEIDP:ESNTNYNQKFKGATFLVDISSSTAYMOLSLTSEDSAVYYCARGGIDGWY 125

QY 126 AIDYWGQTSVTSS 140
 DB 126 AIDYWGQTLVTSS 140

RESULT 5
 W83041
 ID W83041 standard; Protein: 464 AA.
 XX
 AC W83041;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas Mab HFE7A heavy chain.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 CDR.
 XX
 OS Mus musculus
 XX

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 20..464
 FT /label= Mat_protein
 FT Region 20..140
 FT /label= Variable
 FT Region 141..464
 FT /label= Constant
 FT Region 50..54
 FT /label= CDR_H1
 FT /note= "Claim 9"
 FT Region 69..84
 FT /label= CDR_H2
 FT /note= "Claim 9"
 FT Region 118..128
 FT /label= CDR_H3
 FT /note= "Claim 9"
 XX

PN AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 XX 01-APR-1997; 97JP-0082953.
 XX 25-JUN-1997; 97JP-0169088.
 XX

(SANY) SANKYO CO LTD.
 AKIO S. Hideyuki H. Hiroko Y. Jun O. Kimihisa I;
 Masahiko O. Nobufusa S. Shin Y. Tohru T;
 WPI: 1998-543440/47.
 N-PSDB; V71029.
 New antibodies and proteins bind conserved epitope of Fas antigen -
 used to evaluate drugs in animal models and to treat Fas-associated
 diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 myocarditis, hepatitis and AIDS
 Reference Example 4; Page 187-188; 292pp; English.
 This is the amino acid of the heavy chain of murine anti-human Fas
 monoclonal antibody HFE7A. cDNA (see V70129) encoding the heavy
 chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
 RNA by RT-PCR (see V70125-26). The invention provides humanised
 HFE7A antibodies (see W83031-37) produced by CDR grafting. These
 antibodies are capable of inducing apoptosis in abnormal cells
 expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 cells. They are used to evaluate, in animal models, treatments of
 diseases that involve Fas/Fas ligand interactions, and also to treat
 such diseases, including autoimmune disease (e.g. systemic lupus
 erythematosus, Hashimoto's disease, graft versus host disease,
 Sjogren syndrome, pernicious anaemia, Crohn's disease, rheumatoid
 scleroderma, Goodpasture syndrome, Crohn's disease, myasthenia
 arthritis, autoimmune haemolytic anaemia, sterility, thrombopenia
 purpura, multiple sclerosis, Basedow's disease, thrombopenia purpura
 and insulin-dependent diabetes, allergies, atopy, arteriosclerosis,
 myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 Sequence 464 AA;
 SQ

Query Match 81.2%; Score 615; DB 19; Length 464;
 Best Local Similarity 84.3%; Pred. No. 3.8e-43;
 Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTSVHVSQVQLQPGAEVLKPGTSTVKLSCKGSGYFTFTSYMMHWKQRP 60
 DB 1 MGWSCILFLVSTSVHVSQVQLQPGAEVLKPGTSTVKLSCKGSGYFTFTSYMMHWKQRP 60

QY 61 GQGLEWIGEIDPSESTNTNQNPKGKATLTVDISSSTAYMOLSLTSEDSAVYYCARGG 120
 DB 61 GQGLEWIGEIDPSESTNTNQNPKGKATLTVDISSSTAYMOLSLTSEDSAVYYCARGG 120

QY 121 DGWDYALDYWGQTSVTSS 140
 DB 121 YSNWYFDWGTGTTVSS 140

RESULT 6
 B14747
 ID B14747 standard; Protein: 464 AA.
 XX
 AC B14747;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Mouse anti-Fas antibody HFE7A heavy chain.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; complementarity determining region; CDR; human Fas;
 KW Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; heavy chain.
 XX
 OS Mus musculus.
 XX

PN JP2000169393-A.
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; A72108.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 PS Example 4; Page 67-68; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanized version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. The present sequence represents the
 CC heavy chain of the murine anti-human Fas monoclonal antibody HFE7A,
 CC which is produced by hybridoma HFE7A (FERM-BP-5828).
 XX
 SQ Sequence 464 AA;

Query Match 81.2%; Score 615; DB 21; Length 464;
 Best Local Similarity 84.3%; Pred. No. 3.8e-43;
 Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MGWSCITILFLVSTATSVHSQVLOQPQAEVLKPKTSVKLSCKGCGYFTSYMMHWVKQRP 60
 Db 1 mgwscilflvatatgtnyngqkfgkatltvdtssstaysaymltsedsavyycaarnrd 60
 QY 61 GOGLEWIGEIDPSESNTYNGKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Db 61 ggglewigeidpsdsyngnqkfgkatltvdtssstaysaymltsedsavyycaarnrd 120
 QY 121 DGWDYADYWGQGSTVTVSS 140
 Db 121 ysnwnyfdwvgtgtvtvss 140

RESULT 7
 W90897
 ID W90897 standard; Protein; 464 AA.
 XX
 AC W90897;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Murine anti-Fas antibody HFE7A heavy chain protein.
 XX
 KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;

KW insulins dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Mus musculus.
 XX EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 XX 29-SEP-1999; 99EP-0307711.
 XX
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI: 2000-258930/23.
 DR N-PSDB; A11546.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Example reference 4; Page 100-102; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas monoclonal antibody HFE7A heavy chain described in the
 CC method of the invention.
 XX
 SQ Sequence 464 AA;

Query Match 81.2%; Score 615; DB 21; Length 464;
 Best Local Similarity 84.3%; Pred. No. 3.8e-43;
 Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MGWSCITILFLVSTATSVHSQVLOQPQAEVLKPKTSVKLSCKGCGYFTSYMMHWVKQRP 60
 Db 1 mgwscilflvatatgtnyngqkfgkatltvdtssstaysaymltsedsavyycaarnrd 60
 QY 61 GOGLEWIGEIDPSESNTYNGKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
 Db 61 ggglewigeidpsdsyngnqkfgkatltvdtssstaysaymltsedsavyycaarnrd 120
 QY 121 DGWDYADYWGQGSTVTVSS 140
 Db 121 ysnwnyfdwvgtgtvtvss 140

```
RESULT 8
R76088
ID R76088 standard; Protein: 464 AA.
XX
AC R76088;
XX
DT 21-NOV-1995 (first entry)
XX
DE MAb 55.1 heavy chain.
XX
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Sig_peptide
FT /label= Mat_protein
FT /note= "claim 3, page 97-98"
XX
PN W09515382-A.
XX
PD 08-JUN-1995.
XX
PF 29-NOV-1994; 94WO-GB02610.
XX
PR 03-JUN-1994; 94GB-0011089.
PR 03-DEC-1993; 93GB-0024819.
XX
PA (ZENE ) ZENEKA LTD.
XX
PI Blakey DC, Root C, Copley CG, Hall SM, Paterson DS;
PI Rose MS, Wr. ght AF;
XX
DR WPI; 1995-215262/28.
DR N-PSDB; Q94017.
XX
PT Antigen binding structures containing CDRs recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the
PT diagnosis and therapy of cancer
XX
PS Disclosure; Fig.15; 12lpp; English.
XX
CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
CC antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036)
CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or
CC V-min humanised 55.1 constructs have been expressed in myeloma
CC cells and E. coli.
XX
SQ Sequence 454 AA;

Query Match 78.9%; Score 597; DB 16; Length 464;
Best Local Similarity 80.0%; Pred. No. 1.1e-41;
Matches 112; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGNSCIIFLVSTATSVHSQVQLQQGAEIVKPGTSLVKLSCKGYGTFTSYMMHWKQRP 60
DB 1 mgwsyilflvatgtdvhsqvlqpgaaelvkgasvqlsckasgytftgywhwvkqr 60
QY 61 GQGLEWTJEDIPSESNYNNOKYKATLIVDSSSTAYMQLSSLSEDSAVYVCARGGY 120
DB 61 gqglew|jevnps|grsdyn|ekfn|katltv|dkssttaymqlssltsedsav|ycarera 120
QY 121 DGWDYAIQYWGQGTSTVTVSS 140
DB 121 ygyddamdywgqgtstvtvss 140
```

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Db 121 ygyddamdywgqgtstvtvss 140

RESULT 9
W24025
ID W24025 standard; Protein: 443 AA.
XX
AC W24025;
XX
DT 04-MAR-1998 (first entry)
XX
DE Single chain antigen hybrid receptor.
XX
KW Hybrid receptor; single chain antigen; gene therapy; diagnosis;
KW signal conduction; receptor; control region.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= leader_peptide
FT /note= "single chain antigen hybrid receptor"
FT Region 20..444
FT /label= VH_B_1-8
FT /note= "variable heavy chain region of B1-8 antibody"
FT Region 140..154
FT /label= (Gly_Ser)3
FT /note= "linker region"
FT Region 155..264
FT /label= VL_B_1-8
FT /note= "variable light chain region of B1-8 antibody"
FT Region 265..309
FT /label= CD_8-alpha_hinge
FT Domain 310..330
FT /label= transmembrane_domain
FT Domain 331..444
FT /label= cytoplasmic_domain
XX
PN W09720938-A2.
XX
PD 12-JUN-1997.
XX
PF 03-DEC-1996; 96WO-DE02334.
XX
PR 05-DEC-1995; 95DE-4045351.
XX
PA (UYPR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
XX
PI Kulmburg P, Mertelsmann R, Rosenthal F;
XX
DR WPI; 1997-319784/29.
XX
DR N-PSDB; T77137.
XX
PT Cells with hybrid receptor having extracellular and intracellular
PT regions of different origins - useful in gene therapy and diagnosis
PT of tumours
XX
PS Example 3; Fig 4; 46pp; German.
XX
CC This sequence represents a novel single chain antigen hybrid receptor
CC (HR) and contains an extracellular domain specific for the hapten
CC 4-hydroxy-3-iodo-3-nitrophenyl acetate (NIP) coupled to the CD8-alpha
CC region and the transmembrane and signal-conducting intracellular parts
CC of the CD3-zeta molecule. Such hybrid receptors comprise a receptor part
CC localised on the outside of the cell and specific to a particular signal
CC molecule and a receptor part originating from another receptor, localised
CC on the inside of the cell and capable of setting off a signal inside the
CC cell. The cell should also contain at least one other gene construct with
CC a control region which can interact with the signal sent out by the
CC hybrid receptor and thereby control expression of a transgene bound to
CC this control region. Such cells are useful in gene therapy or for
```

CC diagnostic purposes.

XX Sequence 443 AA;

Query Match 78.5%; Score 594.5; DB 18; Length 443;

Best Local Similarity 80.7%; Pred. No. 1.7e-41;

Matches 113; Conservative 6; Mismatches 20; Indels 1; Gaps 1;

QY 1 MGWSCIIILFLVSTATSVHVSQVLOQPAGELVKPGTSVKLSCKGYGYTFTSYMMHWVKQRP 60

DB 1 mgwscimlflaatatgshgqvlqsgaelvkgasvklckasgytftsywmhwvkqr 60

QY 61 GQGLEWIGEIDPSESNTNKNOKFKGKATLTVDLSSSTAYMQLSLTSSESAVYYCARGY 120

DB 61 grglewigrdpsnggkynekfkskatltvdkspsstaymqsltsedsavyycaarydy 120

QY 121 DGWDYAIIDYWGQGTSTVSS 140

DB 121 ygsy-fdywgggtttvss 139

RESULT 10

R27049 ID R27049 standard; Protein; 140 AA.

XX AC R27049;

XX DT 01-MAR-1993 (first entry)

XX DE VH425 antibody cloned into pUC18.

XX KW Monoclonal antibody; complementarity determining region; framework;

XX KW antigens: tumour; melanoma; carcinoma; glioma; light; heavy;

XX KW variable; chain.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Peptide 1..19

XX FT Protein /note= "signal peptide"

XX FT Region 20..140

XX FT Region /note= "mature protein"

XX FT Region 50..54

XX FT Region /label= CDR1

XX FT Region 69..85

XX FT Region /label= CDR2

XX FT Region 118..129

XX FT Region /label= CDR3

XX PN W09215683-A.

XX PD 17-SEP-1992.

XX PF 04-MAR-1992; 92WO-EP00480.

XX PR 06-MAR-1991; 91EP-0103389.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Bendig MM, Kettleborough CA, Saldanha J;

XX DR WPI; 1992-331729/40.

XX DR N-PSDB; Q28739.

XX PT Human monoclonal antibodies binding to human receptors - for

XX PT treatment and diagnosis of tumours, e.g. melanoma and carcinoma

XX PS Disclosure; Fig 2; 89pp; English.

XX CC The variable heavy chain of monoclonal antibody 425 was prepnd. from

XX CC a synthetic cDNA sequence in which mutations had been made to the 5'

XX CC and 3' ends to allow for cloning into HCMV expression vectors.

CC Donor splice sites were recreated in the 3' flanking regions to
 CC allow correct splicing of the variable and constant regions. The
 CC 5' sequence was altered to introduce an initiation codon.
 CC The cloned antibody may be used in the prodn. of reshaped or
 CC humanised antibodies which are less immunogenic than native
 CC antibodies and may be used to combat e.g. glioma, melanoma or
 CC carcinoma. See also R27299-300 and R27037-41.

XX Sequence 140 AA;

Query Match 77.8%; Score 589; DB 13; Length 140;

Best Local Similarity 80.7%; Pred. No. 1.5e-41;

Matches 113; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVSTATSVHVSQVLOQPAGELVKPGTSVKLSCKGYGYTFTSYMMHWVKQRP 60

DB 1 mgwscimlflaatatgshgqvlqsgaelvkgasvklckasgytftshmwvkvkra 60

QY 61 GQGLEWIGEIDPSESNTNKNOKFKGKATLTVDLSSSTAYMQLSLTSSESAVYYCARGY 120

DB 61 ggglewigeifnpsngrtnynekfkskatltvdksststaymqsltsedsavyycaardy 120

QY 121 DGWDYAIIDYWGQGTSTVSS 140

DB 121 dydgryfdywggtttltvss 140

RESULT 11

P70624 ID P70624 standard; protein; 136 AA.

XX AC P70624;

XX DT 09-APR-1991 (first entry)

XX DE Sequence encoded by anti-hepatitis B heavy chain variable region in

XX DE PING2006E.

XX KW Chimeric antibody; Anti-cancer antibody.

XX PN W08702671-A.

XX PD 07-MAY-1987.

XX PF 27-OCT-1986; 86WO-US02269.

XX PR 01-NOV-1985; 85US-0793980.

XX PA (ITGE-) INT GENETIC ENG INC.

XX PA (ROBI/) ROBINSON R R.

XX PI Robinson RR, Liu AY, Horwitz AH, Wall R;

XX DR WPI; 1987-136004/19,

XX DR N-PSDB; N70967, N70968.

XX PT Prodn. of immunoglobulin chains and molecules - is by recombinant

XX PT DNA procedures, with chimeric antibodies etc. related to cancer

XX PT specific antigens.

XX PS Example; Fig 12B; 126pp; English.

XX CC The patentors claim a chimeric antibody molecule comprising 2 light

XX CC chains and 2 heavy chains, each comprising a constant human region

XX CC and a variable non-human region. Coding sequences for the Ig chains

XX CC are also claimed. The invention provides consensus sequences of

XX CC light and heavy chain J regions useful in the design of

XX CC oligonucleotides (UIGs) for use as primers or probes for cloning

XX CC immunoglobulinlight or heavy chain mRNAs or genes. Depending on the

XX CC nature of design of a particular UIG, it may be capable of

XX CC hybridizing to all Ig mRNAs or genes containing a single specific J

XX CC sequence. UIG denotes universal immunoglobulin gene.

```

XX SQ Sequence 1:6 AA;
Query Match 77.4%; Score 586; DB 8; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.6e-41;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIIILFLVSTATSVHSGVOLQOPGAELVKPGTSVKLSCKGYGTYFTSYWMHWKQRP 60
Db 1 mgwsyililflvatardvhsqvlqqpgaelvkpgasvkscasgytftsywmhwkqrp 60

QY 61 GQGLEWIGETIDPSESNTNQNKFGRATLTVDISSTAYMQLSSLTSEDSAVVYCARGY 120
Db 61 ggglwdwigeinpsngrtnynekfkskatltvdkssstaymqilssltseedsavvyccasydy 120

QY 121 DGWDYAIDYWGQGTSTVSS 140
Db 121 d-w---faywgggtlvtvss 136

RESULT 12
W10584
ID W10584 standard; Protein; 136 AA.
XX AC W10584;
XX DT 21-OCT-1997 (first entry)
XX DE Anti-hepatitis B heavy chain variable region.
XX KW Immunoglobulin G; IgG; heavy chain; recombinant production;
KW antibody; passive immunisation; serum sickness; anaphylactic shock;
KW immunoassay; imaging; reagent; complement mediated lysis;
KW therapy; hepatitis B virus; variable region; HBV.
XX OS Mus spp.
XX PN US5595898-A.
XX PR 21-JAN-1997.
XX PF 01-NOV-1985; 85US-0793980.
XX PR 29-MAR-1990; 90US-0501092.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 27-OCT-1986; 86WO-US02269.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 08-DEC-1992; 92US-0987555.
XX PR 18-AUG-1994; 94US-0299085.
XX PA (XOMA ) XOMA CORP.
XX PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX WP: 1997-107579/10.
XX DR N-PSDB; T36303, T36304.
XX Nucleic acid encoding immunoglobulin fragment - comprising
XX di:clstronic transcription unit with pectate lyase signal sequences
XX Example; Fig 12B; 95pp; English.
XX CC The cDNA sequence encoding present anti-hepatitis B heavy chain
CC variable sequence, was used in the preparation of a novel
CC polynucleotide molecule encoding an Ig fragment. The DNA
CC molecule comprises 2 DNA sequences encoding 2 pectate lyase
CC secretion signal sequences respectively linked to a DNA sequence
CC encoding an Ig Fd molecule or Ig light chain, operably linked to a
CC single prokaryotic promoter so as to form a dicistronic
CC transcription unit, provided that the Ig fragment can bind an

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CC antigen and is produced and secreted by an E. coli host cell when
 CC the nucleic acid molecule is expressed in the host cell.
 CC The polynucleotide molecule is used for the production of
 CC recombinant antibodies, which can be used for passive immunisation
 CC without negative immune reactions (e.g. serum sickness and
 CC anaphylactic shock), in labelled forms as immunoassay or imaging
 CC reagents, in complement mediated lysis and for therapeutic
 CC purposes when coupled to a toxin or other therapeutic agent.

XX Sequence 136 AA;

Query Match 77.4%; Score 586; DB 18; Length 136;
 Best Local Similarity 81.4%; Pred. No. 2.6e-41;
 Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIIILFLVSTATSVHSGVOLQOPGAELVKPGTSVKLSCKGYGTYFTSYWMHWKQRP 60
 Db 1 mgwsyililflvatardvhsqvlqqpgaelvkpgasvkscasgytftsywmhwkqrp 60
 QY 61 GQGLEWIGETIDPSESNTNQNKFGRATLTVDISSTAYMQLSSLTSEDSAVVYCARGY 120
 Db 61 ggglwdwigeinpsngrtnynekfkskatltvdkssstaymqilssltseedsavvyccasydy 120
 QY 121 DGWDYAIDYWGQGTSTVSS 140
 Db 121 d-w---faywgggtlvtvss 136

RESULT 13
 W16340
 ID W16340 standard; Protein; 136 AA.

XX AC W16340;
 XX DT 04-SEP-1997 (first entry)
 XX DE Mouse-human chimaeric anti-hepatitis B heavy chain.
 XX KW Antibody engineering; heavy chain; light chain; chimaeric antibody;
 KW passive immunisation; diagnosis; hybridoma; hepatitis B virus;
 KW HBsAg; PING2006E; PING2012E.

XX Chimaeric Mus sp.;

XX Chimaeric Homo sapiens.

XX Key Location/Qualifiers

XX Protein 1..114 /label= VH

XX Peptide 115..117 /note= "mouse heavy chain variable region"

XX /label= J

XX Misc-difference 117 /note= "human J region"

XX /note= "alteration from mouse to human sequence
 (Ala to Ser) introduced in the chimaeric
 J region"

XX US5618920-A.

XX 08-APR-1997.

XX 01-NOV-1985; 85US-0793980.

XX 29-MAR-1990; 90US-0501092.

XX 01-NOV-1985; 85US-0793980.

XX 27-OCT-1986; 86WO-US02269.

XX 24-JUL-1987; 87US-0077528.

XX 11-JAN-1988; 88US-0142039.

XX 17-APR-1992; 92US-0870404.

XX 29-APR-1994; 94US-0235225.

XX (XOMA) XOMA CORP.


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XX
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
XX Wall R, Wilcox GL;
XX
DR WPI; 1997-225473/20.
DR N-PSDB; T70857-58.
XX
XX Secretable immunoglobulin heavy and light chain fragments - capable
PT of assembling into chimeric antibodies, useful for e.g. passive
PT immunisation, diagnosis, etc
XX
XX Example 2; Fig 12B; 96pp; English.
XX
XX A chimeric polypeptide (W16340) comprises a mouse anti-HBsAg
CC heavy chain variable region (derived from hybridoma ATCC CRL8017)
CC and a human J region sequence. It is encoded by DNA sequences in
CC plasmids pING2006E (T70857) or pING2012E (T70858). A complete
CC polypeptide, comprising the mouse anti-HBsAg heavy chain
CC variable region and human constant region, has been expressed in
CC bacterial and transfected mouse cell hosts. Gene amplification has
CC allowed prodn. of chimeric heavy chain.
XX
XX Sequence 136 AA;
XX
XX Query Match 77.4%; Score 586; DB 18; Length 136;
XX Best Local Similarity 81.4%; Pred. No. 2.6e-41;
XX Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;
XX
XX QY 1 MGWSCIIILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGTYTTSYMMHWKORP 60
XX Db 1 mgwsyllilflvatardvhsqvlqpgaelvkgasvkscasgytftsymbhwkqr 60
XX
XX QY 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMOLSLTSDSVAVYVCARGGY 120
XX Db 61 gqglwdwgeinpsngrtrnynefkfskatltvdkssstaymqsltsdsavvyccasydy 120
XX
XX QY 121 DCWDYADYWGQGTSTVTVSS 140
XX Db 121 d-w---faywggtlvtvss 136
XX
XX RESULT 14
XX W10239
XX ID W10239 standard; Protein; 136 AA.
XX AC W10239;
XX
XX DT 05-AUG-1997 (first entry)
XX
XX DE Chimeric anti-hepatitis heavy chain from pING2006E.
XX KW Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
XX KW protein production; human; constant region; passive immunisation; toxin;
XX KW serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm;
XX KW antibody; Ig; heavy-chain; hepatitis; mouse; chimera.
XX
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Mus musculus.
XX
XX PN US5576195-A.
XX
XX PD 19-NOV-1996.
XX
XX PF 01-NOV-1985; 85US-0793980.
XX
XX PR 29-MAR-1990; 90US-0501082.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 27-OCT-1986; 86WO-US02269.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 08-DEC-1992; 92US-0967555.
XX PR 22-FEB-1993; 93US-0020671.

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PR 09-DEC-1994; 94US-0357234.
XX (XOMA ) XOMA CORP.
XX
XX PI Better M, Lei S, Robinson RR, Wilcox GL;
XX
XX DR WPI; 1997-011254/01.
XX DR N-PSDB; T51039.
XX
XX PT Improved prodn. of protein in Gram -ve bacteria using signal
XX sequence - from pectate lyase to ensure transport of protein from
XX the cytoplasm, esp. for prodn. of antibodies
XX
XX Example 2; Fig 12B; 86pp; English.
XX
XX This sequence represents a fragment of the human-mouse chimeric
XX anti-hepatitis heavy chain encoded by the gene contained within
XX pING2006E. pING2006E was used in the method of the invention to express
XX the chimeric heavy chain. The method of the invention is for the
XX production of a protein in a Gram-negative bacterium. The method improves
XX on current techniques, by using a vector including DNA encoding the
XX pectate lyase signal sequence (see T51034), attached to the sequence
XX encoding the protein for production. The method is especially used to
XX make immunoglobulins (Ig), particularly those with a human constant
XX region, suitable for passive immunisation (without risk of serum sickness
XX or anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig may
XX also be used therapeutically, optionally coupled to toxins, etc.
XX Alternatively the protein to be produced is the sweetener thaumatin. The
XX presence of this signal sequence means that the protein is exported from
XX the cytoplasm and can be recovered from the culture medium or periplasm,
XX in active and correctly folded form. The method allows the class of any
XX antibody to be switched, e.g. most human-human Ig are of M class, easily
XX reduced and aggregated, and these can now be changed to G, A or E
XX classes.
XX
XX SQ Sequence 136 AA;
XX
XX Query Match 77.4%; Score 586; DB 18; Length 136;
XX Best Local Similarity 81.4%; Pred. No. 2.6e-41;
XX Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;
XX
XX QY 1 MGWSCIIILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGTYTTSYMMHWKORP 60
XX Db 1 mgwsyllilflvatardvhsqvlqpgaelvkgasvkscasgytftsymbhwkqr 60
XX
XX QY 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMOLSLTSDSVAVYVCARGGY 120
XX Db 61 gqglwdwgeinpsngrtrnynefkfskatltvdkssstaymqsltsdsavvyccasydy 120
XX
XX QY 121 DCWDYADYWGQGTSTVTVSS 140
XX Db 121 d-w---faywggtlvtvss 136
XX
XX RESULT 15
XX W47510
XX ID W47510 standard; Protein; 136 AA.
XX AC W47510;
XX
XX DT 05-JUN-1998 (first entry)
XX
XX DE Human anti-hepatitis antibody heavy chain.
XX
XX KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
XX KW immunoglobulin fragment production; Ig fragment production;
XX KW monoclonal antibody L6; human lung carcinoma cell.
XX
XX OS Homo sapiens.
XX
XX PN US5698435-A.
XX
XX

```


Sat Apr 14 08:10:22 2001

us-08-700-737-15.rag

Page 11

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:49 ; Search time 117.03 Seconds
(without alignments)
192.426 Million cell updates/sec

Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGWDYADYWGQTSVTYSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main.*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
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19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
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23: /cgn2_6/ptodata/2/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	757	100.0	140	11	US-08-700-737-15
2	730	96.4	137	11	US-08-700-737-4
3	713	94.2	144	11	US-08-700-737-2
4	658	86.9	121	11	US-08-700-737-9
5	635	83.9	180	11	US-08-700-737-19
6	615	81.2	464	14	US-09-053-583-9
7	615	81.2	464	18	US-09-408-646-9
8	615	81.2	464	18	US-09-499-662-9
9	589	77.8	140	8	US-08-487-165-24
10	583	77.0	143	10	US-08-692-084-26

11	583	77.0	143	11	US-08-779-784-26
12	583	77.0	143	17	US-09-322-862-26
13	582	76.9	466	20	US-09-898-705-11
14	572	75.6	121	11	US-08-700-737-55
15	567	74.9	470	18	US-09-408-646-143
16	567	74.9	470	18	US-09-499-662-143
17	565	74.6	470	18	US-09-408-646-145
18	565	74.6	470	18	US-09-499-662-145
19	564	74.5	470	14	US-09-053-583-117
20	564	74.5	470	18	US-09-408-646-117
21	564	74.5	470	18	US-09-408-646-147
22	564	74.5	470	18	US-09-499-662-117
23	564	74.5	470	18	US-09-499-662-147
24	556	73.4	145	14	US-09-053-583-75
25	556	73.4	145	18	US-09-408-646-75
26	556	73.4	145	18	US-09-499-662-75
27	556	73.4	470	14	US-09-053-583-89
28	556	73.4	470	18	US-09-408-646-89
29	556	73.4	470	18	US-09-499-662-89
30	549	72.5	140	8	US-08-475-815-11
31	549	72.5	140	13	US-08-921-060-11
32	549	72.5	137	12	US-08-238-741-4
33	548.5	72.5	137	12	US-08-864-983A-21
34	545	72.0	470	18	US-09-408-646-157
35	545	72.0	470	18	US-09-499-662-157
36	544.5	71.9	139	5	US-08-137-117B-35
37	544.5	71.9	139	5	US-08-137-117C-35
38	544.5	71.9	139	15	US-09-114-285-35
39	544.5	71.9	139	15	US-09-114-285A-35
40	541	71.5	140	8	US-08-475-813-6
41	536	70.8	119	4	US-08-073-967-44
42	536	70.8	119	9	US-08-553-497-12
43	532	70.3	138	6	US-08-286-754-78
44	532	70.3	138	8	US-08-408-724-78
45	532	70.3	138	21	US-09-753-436-78

ALIGNMENTS

RESULT 1

US-08-700-737-15
; Sequence 15, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; TITLE OF INVENTION: INTEGRIN
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-i0

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-700-737-15

Query Match 100.0%; Score 757; DB 11; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.4e-65;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGWSCIIIFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGSGYGTFTSYWMHWVKQRP 60
Db 1 MGWSCIIIFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGSGYGTFTSYWMHWVKQRP 60
Qy 61 GQGLEWICEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGY 120
Db 61 GQGLEWICEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGY 120
Qy 121 DGWDYAIIDYWGQTSVTSS 140
Db 121 DGWDYAIIDYWGQTSVTSS 140

RESULT 2
US-08-700-737-4
Sequence 4, Application US/08700737
GENERAL INFORMATION:
APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-700-737-4

Query Match 96.4%; Score 730; DB 11; Length 137;
Best Local Similarity 98.5%; Pred. No. 1.7e-62;
Matches 135; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGWSCIIIFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGSGYGTFTSYWMHWVKQRP 60
Db 1 MGWSCIIIFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGSGYGTFTSYWMHWVKQRP 60
Qy 61 GQGLEWICEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGY 120
Db 61 GQGLEWICEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGY 120
Qy 121 DGWDYAIIDYWGQTSVT 137
Db 121 DGWDYAIIDYWGQTSVT 137

RESULT 3
US-08-700-737-2
Sequence 2, Application US/08700737
GENERAL INFORMATION:
APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-700-737-2

Query Match 94.2%; Score 713; DB 11; Length 144;
Best Local Similarity 99.3%; Pred. No. 7.7e-61;
Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 ILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGSGYGTFTSYWMHWVKQRPQGLEW 66
Db 7 IXFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGSGYGTFTSYWMHWVKQRPQGLEW 66
Qy 67 IGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGTDGNDYA 126
|||||

Db 67 IGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYDGDWYA 126
QY 127 IDYWGQGTSTVTSS 140
Db 127 IDYWGQGTSTVTSS 140

RESULT 4
US-08-700-737-9
; Sequence 9, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700.737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-700-737-9

Query Match 86.9%; Score 658; DB 11; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2e-55;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 QVQLQPGAEVLKPKTSVKLSCKGKGYTFTSYMMHWKQRPQGQLEWIGETIDPSESNTNY 79
Db 1 QVQLQPGAEVLKPKTSVKLSCKGKGYTFTSYMMHWKQRPQGQLEWIGETIDPSESNTNY 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYDGDWYDAIDYWGQGTSTVTS 139
Db 61 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYDGDWYDAIDYWGQGTSTVTS 120
QY 140 S 140
Db 121 S 121

RESULT 5
US-08-700-737-19
; Sequence 19, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700.737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-700-737-9

Query Match 83.9%; Score 635; DB 11; Length 180;
Best Local Similarity 86.7%; Pred. No. 3.1e-53;
Matches 117; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 6 IILFLVSTATSVHSQVQLQPGAEVLKPKTSVKLSCKGKGYTFTSYMMHWKQRPQGQLE 65
Db 6 VILFLVSTATSVHSQVQLQPGAEVLKPKTSVKLSCKGKGYTFTSYMMHWKQRPQGQLE 65
QY 66 WIGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYDGDWY 125
Db 66 WIGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYDGDWY 125
QY 126 AIDYWGQGTSTVTSS 140
Db 126 AIDYWGQGTSTVTSS 140

RESULT 6
US-09-053-583-9
; Sequence 9, Application US/09053583A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Ohtsumi, Jun
; APPLICANT: Ohtsuki, Masahiko
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Yoshida, Hiroko
; APPLICANT: Shiraishi, Akio
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126/HG

; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700.737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-19

Query Match 83.9%; Score 635; DB 11; Length 180;
Best Local Similarity 86.7%; Pred. No. 3.1e-53;
Matches 117; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 6 IILFLVSTATSVHSQVQLQPGAEVLKPKTSVKLSCKGKGYTFTSYMMHWKQRPQGQLE 65
Db 6 VILFLVSTATSVHSQVQLQPGAEVLKPKTSVKLSCKGKGYTFTSYMMHWKQRPQGQLE 65
QY 66 WIGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYDGDWY 125
Db 66 WIGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYDGDWY 125
QY 126 AIDYWGQGTSTVTSS 140
Db 126 AIDYWGQGTSTVTSS 140

RESULT 6
US-09-053-583-9
; Sequence 9, Application US/09053583A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Ohtsumi, Jun
; APPLICANT: Ohtsuki, Masahiko
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Yoshida, Hiroko
; APPLICANT: Shiraishi, Akio
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126/HG

Sat Apr 14 08:10:23 2001

us-08-700-737-15.rapm

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; CURRENT APPLICATION NUMBER: US/09/053.583A
; CURRENT FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: JP HEI 9-82953
; EARLIER FILING DATE: 1997-04-01
; EARLIER APPLICATION NUMBER: JP HEI 9-169088
; EARLIER FILING DATE: 1997-06-25
; EARLIER APPLICATION NUMBER: JP HEI 9-276064
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-053-583-9

Query Match      81.2%; Score 615; DB 14; Length 464;
Best Local Similarity 84.3%; Pred. No. 7.8e-51;
Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEVLKPGTSVKLSCKGKYGTFTSYMMHWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGWSCIILFLVATATGVHSQVLOQPGAEVLKPGASVKLSCKRASGYTFTSYMMQWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GQGLEWIG:IDPSESNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARGY 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GQGLEWIG:IDPDSYNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARNRD 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 DGWDYALDYWGOGTSVTSS 140
   :: ||||| |||||
Db 121 YSNWYF:VWGTGTTVTSS 140
   :: ||||| |||||

RESULT 7
US-09-408-646-9
; Sequence 9, Application US/09408646A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 990540/HG
; CURRENT APPLICATION NUMBER: US/09/408,646A
; CURRENT FILING DATE: 1999-09-30
; EARLIER APPLICATION NUMBER: JP 10-276881
; EARLIER FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-408-646-9

Query Match      81.2%; Score 615; DB 18; Length 464;
Best Local Similarity 84.3%; Pred. No. 7.8e-51;
Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEVLKPGTSVKLSCKGKYGTFTSYMMHWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGWSCIILFLVATATGVHSQVLOQPGAEVLKPGASVKLSCKRASGYTFTSYMMQWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GQGLEWIG:IDPSESNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARGY 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GQGLEWIG:IDPDSYNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARNRD 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 DGWDYALDYWGOGTSVTSS 140
   :: ||||| |||||
Db 121 YSNWYF:VWGTGTTVTSS 140
   :: ||||| |||||

RESULT 8
US-09-499-662-9
; Sequence 9, Application US/09499662
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/09/499,662
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: US 09/053,583
; EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-499-662-9

Query Match      81.2%; Score 615; DB 18; Length 464;
Best Local Similarity 84.3%; Pred. No. 7.8e-51;
Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEVLKPGTSVKLSCKGKYGTFTSYMMHWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGWSCIILFLVATATGVHSQVLOQPGAEVLKPGASVKLSCKRASGYTFTSYMMQWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GQGLEWIG:IDPSESNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARGY 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GQGLEWIG:IDPDSYNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARNRD 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 DGWDYALDYWGOGTSVTSS 140
   :: ||||| |||||
Db 121 YSNWYF:VWGTGTTVTSS 140
   :: ||||| |||||

RESULT 9
US-08-487-165-24
; Sequence 24, Application US/08487165
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,165
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA: US 07/946,421
; APPLICATION NUMBER:
; FILING DATE: 06-NOV-1992
; PRIOR APPLICATION DATA: WO PCT/EP92/00480
; APPLICATION NUMBER:
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
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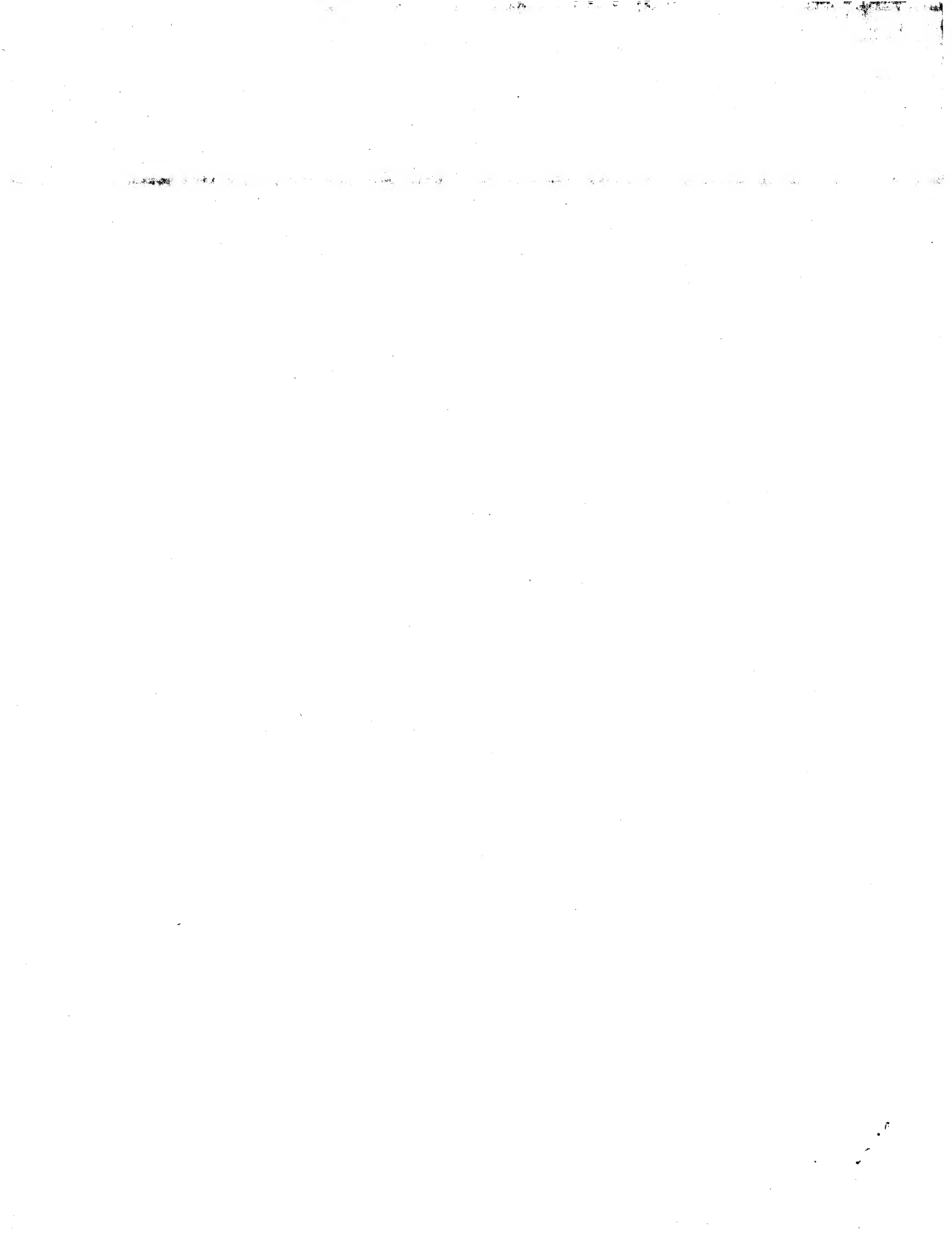

RESULT 10
US-08-692-084-26
; Sequence 26, Application US/08692084
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION USING MONOC
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/692,084
; FILING DATE: 08-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:

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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/692,084
  FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/236,520
  FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Jackson Esq., David A.
  REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 201-487-5800
  TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 26:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 143 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-784-26

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Search completed: April 13, 2001, 17:37:49
Job time: 166 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:56 ; Search time 4.45 Seconds
(without alignments)
54.611 Million cell updates/sec

Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSO.....DGWDYALDYGQTSVTSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7695 seqs, 1735856 residues

Total number of hits satisfying chosen parameters: 7695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_patents_AA_New.*

1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	72.5	140	4	US-08-475-815A-11
2	463	61.2	132	5	US-09-386-658-2
3	282.5	37.3	482	5	US-09-509-031-16
4	242	32.0	240	5	US-09-782-504-4
5	122	16.1	128	4	US-08-475-815A-7
6	107	14.1	155	5	US-09-509-031-11
7	107	14.1	342	5	US-09-509-031-6
8	107	14.1	495	5	US-09-509-031-4
9	69.5	9.2	442	5	US-09-739-449-9534
10	66.5	8.8	914	5	US-09-193-562D-28
11	65	8.6	517	5	US-09-739-449-12328
12	65	8.6	753	1	PCT-US01-09226-51
13	64	8.5	281	5	US-09-739-449-11638
14	63.5	8.4	170	5	US-09-814-950-4
15	63.5	8.4	172	5	US-09-814-950-2
16	62.5	8.3	109	5	US-09-386-658-4
17	62	8.2	757	5	US-09-739-449-11939
18	60.5	8.0	1008	5	US-09-308-453-2
19	60	7.9	240	5	US-09-739-449-12522
20	59.5	7.9	317	5	US-09-706-029-1
21	59.5	7.9	639	5	US-09-739-449-11223
22	59	7.8	574	5	US-09-815-108-7
23	58.5	7.7	342	5	US-09-815-108-20
24	58.5	7.7	379	5	US-09-813-408-6
25	58.5	7.7	448	5	US-09-815-108-6
26	58.5	7.7	472	5	US-09-815-108-5
27	58.5	7.7	504	5	US-09-815-108-8

28 58.5 7.7 504 5 US-09-815-108-15
29 58.5 7.7 504 5 US-09-815-108-17
30 58.5 7.7 504 5 US-09-815-108-19
31 58.5 7.7 509 5 US-09-815-108-3
32 58.5 7.7 529 5 US-09-815-108-2
33 58.5 7.7 594 5 US-09-815-108-22
34 57.5 7.6 418 5 US-09-739-449-10479
35 57.5 7.6 1112 5 US-09-739-449-10300
36 57 7.5 251 5 US-09-739-449-12898
37 56.5 7.5 172 5 US-09-810-264-26
38 56.5 7.5 322 5 US-09-739-449-8302
39 56 7.4 652 5 US-09-813-742-5
40 56 7.4 1144 5 US-09-813-742-3
41 55.5 7.3 215 5 US-09-739-449-10936
42 55.5 7.3 571 5 US-09-809-391-481
43 55.5 7.3 1758 5 US-09-739-449-11627
44 55 7.3 101 5 US-09-809-391-754
45 55 7.3 216 5 US-09-739-449-12644

ALIGNMENTS

RESULT 1
US-08-475-815A-11
; Sequence 11, Application US/08475815A
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 23522-0157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-815A-11

Sequence 15, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 22, Appl
Sequence 10479, A
Sequence 10300, A
Sequence 12898, A
Sequence 26, Appl
Sequence 8302, Ap
Sequence 5, Appl
Sequence 3, Appl
Sequence 10936, A
Sequence 481, App
Sequence 11627, A
Sequence 734, App
Sequence 12644, A

us-08-700-737-15.rapn

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ccWTlgL protein
;
; OTHER INFORMATION: sequence
US-09-509-031-16

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Query Match 37.3%; Score 282.5; DB 5; Length 482;
Best Local Similarity 44.4%; Pred. No. 9.8e-23;
Matches 55; Conservative 27; Mismatches 39; Indels 3; Gaps

QY 19 SQVQLQPGAEVLKPGTSVKLSCKGCGYFTSYWYHHVVKRPGQGLEWIG-GEIDPSESN 70
 Db 30 SEVKLVESGGGLVQPGSLRLSCATSGFTSDFYMEWVRPQPKRLEWIAASRNKGNYT 89

Qy 77 TNYNOKFKGKATLTVDISSTAYMQLSSLTSEDSAVVYCARGYDGDVDAIDYWGQGTSV 1

Dd 90 TEYSASVKGRFTVSRDTSQSILYLQMNALRAEDTAIYYCAR-NYYGSTWCDFVWGAGTTV 14

Qy 137 TVSS 140
|||
Db 149 TVSS 152

RESULT 4
US-09-782-504-4
; Sequence 4, Application US/09782504

APPLICANT: Hellstrom, Ingegerd
Hellstrom, Karl Erik
Bruce, Kim Folger
Schreiber, George J.

McAndrew, Stephen
Siegall, Clay
TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN
CARCINOMAS

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300

STATE: Washington
COUNTRY: USA
ZIP: 98104

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SERIAL NUMBER: Release #1 0
VERSION: #1 25

```

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,504
; FILING DATE: 12-Feb-2001
; CLASSIFICATION: <Unknown>
;

```

ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 840065.405D3

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:

```

;
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
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US-09-782-504-4

Query Match 32.0%; Score 242; DB 5; Length 240;
Best Local Similarity 47.9%; Pred. No. 6.4e-19;
Matches 58; Conservative 24; Mismatches 31; Indels 8; Gap

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Query Match          72.5%; Score 549; DB 4; Length 140;
Best Local Similarity 75.7%; Pred. No. 9.1e-51;
Matches 106; Conservative 10; Mismatches 24; Indels 0; Gaps 0;
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a

1	MGWSCIILFLVSTATSVHSQVOLQQPAELVKPGTSVKLSCKGCGYTFTSYNMHHVTKRP	60	
	:		
b	1	MGWSLILI FLVAVATRVLSQLVOLQQPAELVKPGASVKNMSCKASGYTFTSYNMHHVYKQTP	60

[illegible]

121 DGWDYAIL YWGQGTSTVTS 140
 | | : | | | | | :
 121 YGGDWYFN YWGAGTTVTS 140

RESULT 2
S-09-386-658-2 Application US/09386658

GENERAL INFORMATION:
 APPLICANT: Erlanger, Bernard
 APPLICANT: Chen, Bi-Xing
 TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES

FILE REFERENCE: 0373-34182/JPW/SNS/MVM
CURRENT APPLICATION NUMBER: US/09/386,658
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ : D NOS: 4

SOFTWARE, FUJITSU VISION 310
SEQ ID NO 2
LENGTH: 132
TYPE: PRT

S-09-386-658-2

Best Local Similarity 65.0%; Pred No. 6e-42;
Matches 91; Conservative 12; Mismatches 29; Indels 8; Gaps 1

1 MGCSWGM.FLLSITAGVHCQVHIQQSGPELVPGASVKISCKTSGYVFSSWNWVKQRP 60
61 GCGI.FWT:FIQDPSFNTNYNOKFKGKATLTVDIISSTAYMQLSSLTSDSDSAVYVCARGY 120

bb 61 GGGLKWI:RIYPGNGNTNYYNEKFGKATLTADKSSNTAYMQLSSLTSYDVSAYFCATSS- 119
vv 121 DGWDYAIYWGQGTSTVTSS 140

db 120 -----YWGQGLTVSA 132

US-09-509-031-16
Sequence 16, Application US/09509031
GENERAL INFORMATION:

APPLICANT: Suss, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Trautlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME

FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031
CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 16
; LENGTH: 482
; TYPE: PRT

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ORGANISM: *Alcaligenes* sequence

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RESULT      7
US-09-509-031-6
; Sequence 6, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koenigen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TLHL protein
US-09-509-031-6

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? SEQ ID NO 6
? LENGTH: 342
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence:TLHL protein
? OTHER INFORMATION: sequence
? US-09-509-031-6

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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9534

Query Match          9.2%; Score 69.5; DB 5; Length 442;
Best Local Similarity 25.0%; Pred. No. 0.72;
Matches 30; Conservative 11; Mismatches 50; Indels 29; Gaps 6;

QY 28 AELVPGTSVKLSCKGKYFTTSYWMHWKQKPGQGLEHI--GEIDPSESNTNYNQKPKG 85
Db 97 AILPQGLADIAAKGFLVPLGDDTAKVYENYAGKSWVDLGSYKGDGNKAY-FAPPF 155
QY 86 KATLVVDISSSTAYM-----QLSSLTSE---DSAVYIC---ARGGYDGW 123
Db 156 KA-----DVKSLVWYVPENFEAGYKVPESMEDLLKLTQDIVADGGTPWCIGLGGSGATGW 211

RESULT 10
US-09-193-562D-28
; Sequence 28, Application US/09193562D
; GENERAL INFORMATION:
; APPLICANT: Paull, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; TITLE OF INVENTION: Activated Chloride Channel Adhesion Molecules
; FILE REFERENCE: 18617.0052
; CURRENT APPLICATION NUMBER: US/09/193,562D
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 28
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-562D-28

Query Match          8.8%; Score 66.5; DB 5; Length 914;
Best Local Similarity 25.0%; Pred. No. 3.4;
Matches 34; Conservative 17; Mismatches 50; Indels 35; Gaps 7;

QY 11 VSTATSVHSQ--VLOQPGAEVLKVP---GTSVKLSCKGKYFTTSYWMHWKQKPGQGL 64
Db 475 LSSGNGAVSORSIQLESKGLTQNSQWMNGTVIVDSVKGDTFLITW---TTQPPQIL 530
QY 65 EWICEIDPSESNTNYNQKFKGKATLVDISSSTAYMQLSSLTSEDSAVYICARGGYDGD 124
Db 531 LW---DPS-----GQKGG---FVVDKNTKWAYLIQPIAKVGT-----WK 565
QY 125 YALDYGQGTSTVVS 140
Db 566 YSLQASSQTLLTAVTS 581

RESULT 11
US-09-739-449-12328
; Sequence 12328, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 12328
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9534

Query Match          14.1%; Score 107; DB 5; Length 342;
Best Local Similarity 27.3%; Pred. No. 7.4e-05;
Matches 35; Conservative 19; Mismatches 46; Indels 28; Gaps 7;

QY 21 VLOQPGAEVLKPGTSVKLSCKG-----XYFTTSYWMHWKQKPGQ-----LEWIGEID 71
Db 32 VMTQSPDLSLAVSLGERATINCKSSQSVLYSSNKNY-LAWYQKPGQPPKLLIYW----- 85
QY 72 PSESNTNYNQKFKGKATLVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDWYDAIDY-W 130
Db 86 ASTRESGVPRDFSGSG-----SGTDFTLTSSLQAEADVAVYICQ-----VYSTPYSF 133
QY 131 GQGTSTVTV 138
Db 134 GQGTSTVTV 141

RESULT 8
US-09-509-031-4
; Sequence 4, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Taubert, David M.
; APPLICANT: Trautwein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBIOTIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CATAB-TEV
US-09-509-031-4

Query Match          14.1%; Score 107; DB 5; Length 495;
Best Local Similarity 27.3%; Pred. No. 0.00011;
Matches 35; Conservative 19; Mismatches 46; Indels 28; Gaps 7;

QY 21 VLOQPGAEVLKPGTSVKLSCKG-----XYFTTSYWMHWKQKPGQ-----LEWIGEID 71
Db 32 VMTQSPDLSLAVSLGERATINCKSSQSVLYSSNKNY-LAWYQKPGQPPKLLIYW----- 85
QY 72 PSESNTNYNQKFKGKATLVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDWYDAIDY-W 130
Db 86 ASTRESGVPRDFSGSG-----SGTDFTLTSSLQAEADVAVYICQ-----VYSTPYSF 133
QY 131 GQGTSTVTV 138
Db 134 GQGTSTVTV 141

RESULT 9
US-09-739-449-9534
; Sequence 9534, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9534
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	Matches	20; Conservative	11; Mismatches	37; Indels	29; Gaps	1;
Qy	19	SOVQLQIQIGAEIVKPGCTSVKLSCKGYFTTSYWMHWKORPGOGLEWIGEDIPSESNTN	78			
Db	59	TKYQISQIEVYVAAPGESLEVRCLLKDAVISTWKDGVHLGPNRTVLIGE	109			
Qy	79	YNQKFKGIATLTVDISSSTAYMQLSSLTSEDSAVYYC	115			
Db	110	-----YLIQKGATPRDSGLYAC	126			

Search completed: April 13, 2001, 17:37:57
Job time: 173 sec

US-07-946-421-24
; Sequence 24, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
; APPLICANT: Bandig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ham,et-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64.91
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-07-946-421-24

Query Match 77.8%; Score 589; DB 1; Length 140;
Best Local Similarity 80.7%; Pred. No. 4e-47;
Matches 113; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHVSQVLOQPQGAELVKPCTSVKLSCKGCGYTFSTYMMHWVKORP 60
DB 1 MGWSIIILFLVATATDVHVSQVLOQPQGAELVKPGASVKLSCKASGYTFTSYMMHWVKQRA 60

QY 61 GQGLEWIEIDPESENNTYNNOKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARGY 120
DB 61 GQGLEWIEIDPESENNTYNNOKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARGY 120

QY 121 DGWDYAIYWGQGTSTVSS 140
DB 121 DYDGRYFDYWGQGTTLTVSS 140

RESULT 3
PCT-US95-05262-7
; Sequence 7, Application US/08236520
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education Research
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

US-08-236-520-7
; Sequence 7, Application US/08236520
; Patent No. 5591629
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.

Query Match 77.0%; Score 583; DB 1; Length 143;
Best Local Similarity 80.0%; Pred. No. 1.4e-46;
Matches 112; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHVSQVLOQPQGAELVKPGTSVKLSCKGCGYTFSTYMMHWVKORP 60
DB 1 MGWSIIILFLVAAATGVHVSQVLOQPQGTGLVKPGASVKLSCKASGYTFTSYMMHWVKORP 60

QY 61 GQGLEWIEIDPESENNTYNNOKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARGY 120
DB 61 GQGLEWIEIDPESENNTYNNOKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARGY 120

QY 121 DGWDYAIYWGQGTSTVSS 140
DB 121 YGSRNFDYWGQGTTLTVSS 140

RESULT 4
PCT-US95-05262-7
; Sequence 7, Application PC/TUS9505262
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education Research
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

RESULT      5
US-08-137-117D-35
; Sequence 35, Application US/08137117D
; Patent No. 5795965
;
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JF92/00544
; FILING DATE: 24-APR-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084

```

```

RESULT      6
US-08-436-717-35
; Sequence 35, Application US/08436717
; Patent No. 5817790
;
GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
;
TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
;
NUMBER OF SEQUENCES: 158
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JF92/00544
; FILING DATE: 24-APR-1992
;
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: 202)672-5399
TELEX: 90.136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-35

Query Match 71.9%; Score 544.5; DB 2; Length 139;
Best Local Similarity 72.9%; Pred. No. 4.7e-43;
Matches 102; Conservative 13; Mismatches 24; Indels 1; Gaps 1;
QY 1 MGWSCITFLVSTATSVHSGVQLQPGAEELVKPCTSVKLSCKGCGYGTFTSYNHHWVKQRP 60
Db 1 MGWGVF[FLSVTAGVHSGVQLQPGAEELVKPCTSVKLSCKGCGYGTFTSYNHHWVKQRP 60
QY 61 GQLEWIEIDPSESNTYNOKEKGRATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
Db 61 GHLEWIEIDPSESNTYNOKEKGRATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
QY 121 DGWDYALYWGQTSVTSS 140
Db 121 SGY-YAM)YWGQTSVTSS 139

RESULT 7
US-08-476-275-6
Sequence 6, Application US/08476275
Patent No. 5776156
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Lewman, Roland A.
APPLICANT: Reiff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
TITLE OF INVENTION: Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 619 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22311
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099

FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-275-6

Query Match 71.5%; Score 541; DB 1; Length 140;
Best Local Similarity 75.0%; Pred. No. 9.9e-43;
Matches 105; Conservative 10; Mismatches 25; Indels 0; Gaps 0;
QY 1 MGWSCITFLVSTATSVHSGVQLQPGAEELVKPCTSVKLSCKGCGYGTFTSYNHHWVKQRP 60
Db 1 MGWSLILLFLVAVATRVLSQVQLQPGAEELVKAGASVKMSCKASGYTFTSYNHHWVKOTP 60
QY 61 GQLEWIEIDPSESNTYNOKEKGRATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
Db 61 GRLEWIGAIYPOGDTSYNOKEKGRATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTY 120
QY 121 DGWDYALYWGQTSVTSS 140
Db 121 YGGDWYFNWAGCTTTVSA 140

RESULT 8
US-08-553-497A-12
Sequence 12, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCES
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 94104160.0
 ; FILING DATE: 17-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 94118970.6
 ; FILING DATE: 02-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HAMLET-KING, DIANA
 ; REGISTRATION NUMBER: 33,302
 ; REFERENCE/DOCKET NUMBER: MERCK 1726
 ; TELEPHONE: 703-243-6333
 ; TELEFAX: 703-243-6410
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 119 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-553-497A-12

Query Match 70.8%; Score 536; DB 2; Length 119;
 Best Local Similarity 85.1%; Pred. No. 2.3e-42;
 Matches 103; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
 QY 20 OVLOQPGAEVLKPGTSVKLSCKGYGTFTSYMMHVKORPGGGLWGEIDPSESNTNY 79
 DB 1 EVLOQSGAEVLKPGASVKLSCKASGYTFTSYMMHVKORPGGGLWGEIDPDSYTN 60
 QY 80 NQKFKKATLTVDISSTAYMQLSSLTSDSAVYYCARGYDGDVDAIDYWGQTSVTVS 139
 DB 61 NQKFKKATLTVDKSSSTAYMQLSSLTSDSAVYYCARSYGSSHP--DYWGQTSVTVS 118
 QY 140 S 140
 DB 119 S 119

RESULT 9
 US-08-482-882-78
 ; Sequence 78, Application US/08482882
 ; Patent No. 5773218
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Vazeux, Rosemay
 ; TITLE OF INVENTION: ICAM-Related Materials and Methods
 ; NUMBER OF SEQUENCES: 116
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,882
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286,754
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/102,852
 ; FILING DATE: 05-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,266
 ; FILING DATE: 22-JAN-1993
 ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/894,061
 ; FILING DATE: 05-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/889,724
 ; FILING DATE: 26-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,689
 ; FILING DATE: 27-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NO. 5773218and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 32178
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 78:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 138 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-482-882-78

Query Match 70.3%; Score 532; DB 1; Length 138;
 Best Local Similarity 73.6%; Pred. No. 6.5e-42;
 Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;
 QY 1 MGWSCIILFLVSTATSVHSOVLOQPGAEVLKPGTSVKLSCKGYGTFTSYMMHVKORP 60
 DB 1 MXWSXXFXFLSVTAGVHSOVLOQSGAEVLADPGASVAMSKASGFTFTVYMMHVKORP 60
 QY 61 GQGLEWGEIDPSESNTNYNOKFKKATLTVDISSTAYMQLSSLTSDSAVYYCARGY 120
 DB 61 GQGLEWIGYINPNTDYTEYNORFQDKATLTADKSSSTAYMQLSSLTSDSAVYYCARG- 119
 QY 121 DGWDYDAIDYWGQTSVTVS 140
 DB 120 GNSYGLDWGQTSVTVS 138

RESULT 10
 US-08-483-389-78
 ; Sequence 78, Application US/08483389
 ; Patent No. 5811517
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Vazeux, Rosemay
 ; TITLE OF INVENTION: ICAM-RELATED PROTEIN
 ; NUMBER OF SEQUENCES: 118
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,389
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/102,852
 ; FILING DATE: 05-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,266
 ; FILING DATE: 22-JAN-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sub Young J.
; REGISTRATION NUMBER: P-41,337
; REFERENCE/DOCKET NUMBER: 27866/32760
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-0448
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-389-78

Query Match 70.3%; Score 532; DB 2; Length 138;
Best Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGWSCIIILFVSTATSVHSQVQLQPGAEILVKPGTSVKLSCKGKGYFTFTSYMMHWKQRP 60
Db 1 MXWSXXXFLFSVTAGVHSQVQLQSSAELADPGASVKMSCKASGYTFTVYMMHWKQRP 60
QY 61 GQGLEWIEIDPSESNTNNTNMQKFKGKATLTVDISSTAYMQLSLTSEDSAVYYCARGY 120
Db 61 GQGLEWIGYINPNTDYTEYNQRFQDKATLTADKSSSTAYMQLSLTSEDSAVYYCARWG- 119
QY 121 DGWDYATDYWGQGTSTVTVSS 140
Db 120 -GNSYGLDYWGQGTSTVTVSS 138

RESULT 11
US-08-487-113D-78
; Sequence 78, Application US/08487113D
; Patent No. 5837822
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 3300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,113D
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; PRIOR APPLICATION DATA:

; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5837822and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-113D-78

Query Match 70.3%; Score 532; DB 2; Length 138;
Best Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGWSCIIILFVSTATSVHSQVQLQPGAEILVKPGTSVKLSCKGKGYFTFTSYMMHWKQRP 60
Db 1 MXWSXXXFLFSVTAGVHSQVQLQSSAELADPGASVKMSCKASGYTFTVYMMHWKQRP 60
QY 61 GQGLEWIEIDPSESNTNNTNMQKFKGKATLTVDISSTAYMQLSLTSEDSAVYYCARGY 120
Db 61 GQGLEWIGYINPNTDYTEYNQRFQDKATLTADKSSSTAYMQLSLTSEDSAVYYCARWG- 119
QY 121 DGWDYATDYWGQGTSTVTVSS 140
Db 120 -GNSYGLDYWGQGTSTVTVSS 138

RESULT 12
US-08-473-503-78
; Sequence 78, Application US/08473503
; Patent No. 5869262
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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